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OM protein - protein search, using sw model

Run on: April 13, 2004, 13:15:19 ; Search time 60 seconds

(without alignments)
1648.194 Million cell updates/sec

Title: US-09-721-341-2

Sequence: 1819
1 MALKQNSTDYDYENENNG.....VEEPFDSGPTPTSTFSI 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	2	AAW93169 Human HPI
2	1819	100.0	350	2	AAW93169 Human HPI
3	1819	100.0	350	2	AAW93169 Human HPI
4	1819	100.0	350	2	AAW93169 Human HPI
5	1819	100.0	350	2	AAW93169 Human HPI
6	1819	100.0	350	2	AAW93169 Human HPI
7	1819	100.0	350	2	AAW93169 Human HPI
8	1819	100.0	350	2	AAW93169 Human HPI
9	1819	100.0	350	2	AAW93169 Human HPI
10	1819	100.0	350	2	AAW93169 Human HPI
11	1819	100.0	350	2	AAW93169 Human HPI
12	1819	100.0	350	2	AAW93169 Human HPI
13	1819	100.0	350	2	AAW93169 Human HPI
14	1819	100.0	350	2	AAW93169 Human HPI
15	1819	100.0	350	2	AAW93169 Human HPI
16	1819	100.0	350	2	AAW93169 Human HPI
17	1819	100.0	350	2	AAW93169 Human HPI
18	1819	100.0	350	2	AAW93169 Human HPI
19	1819	100.0	350	2	AAW93169 Human HPI
20	1819	100.0	350	2	AAW93169 Human HPI
21	1819	100.0	350	2	AAW93169 Human HPI
22	1819	100.0	350	2	AAW93169 Human HPI
23	1819	100.0	350	2	AAW93169 Human HPI
24	1819	100.0	350	2	AAW93169 Human HPI
25	1819	100.0	350	2	AAW93169 Human HPI

26	862	47.4	164	4	AAW79310 Human pro
27	824	45.3	159	3	AAW41786 Human ORF
28	761	41.8	175	4	AAU18115 Novel hum
29	761	41.8	175	4	AAU18669 Renal and
30	761	41.8	175	4	AAU21655 Novel hum
31	761	41.8	175	4	AAW99976 Human exp
32	761	41.8	175	4	ABD10276 Human cDN
33	761	41.8	175	4	AAU87280 Novel cDN
34	761	41.8	175	4	AAU18361 Human end
35	761	41.8	175	5	ABJ05742 Novel hum
36	761	41.8	175	5	ABP6863 Human pol
37	761	41.8	175	6	ABU97284 Human pol
38	761	41.8	175	7	ADG46296 Human neo
39	689	36.2	358	2	AAW3745 Partial s
40	659	36.2	358	2	AAW21669 Human 7TM
41	659	36.2	358	5	AAU91231 Human 7 t
42	659	36.2	378	2	AAW48724 Human V31
43	659	36.2	378	3	AAW21668 Human 7TM
44	659	36.2	378	4	AAW80114 Human CCR
45	659	36.2	378	4	AAW50859 Human CCR

ALIGNMENTS

RESULT 1

AAW93169 standard; protein; 350 AA.

AAW93169;

24-MAY-1999 (first entry)

Human HPIA041 protein.

HPIA041; G-coupled receptor; disease susceptibility; diagnosis; immunise; treatment; FIA041 protein; gene therapy; immune response; vaccine; HIV-2; inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer; diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; allergy; angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia; benign prostatic hypertrophy; psychotic disorder; neurological disorder; anxiety; manic depression; delirium; dementia; severe mental retardation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; linkage analysis; gene mapping; human.

Homo sapiens.

EP899332-A2.

03-MAR-1999.

17-FEB-1998; 98EP-00301170.

15-AUG-1997; 97US-0055895P.

27-OCT-1997; 97US-00862822.

(SMIK) SMITHKLINE BEECHAM CORP.

Ellis CE;

WPI; 1999-144803/13.

N-PSDB; AAX22557.

New G-coupled receptor (HPIA041) polypeptide and polynucleotide - useful

as diagnostic reagents and for prevention and treatment of cancer, HIV

infections and Parkinson's disease.

Claim 1; Page 22-23; 27pp; English.

This sequence represents a G-coupled receptor, HPIA041 which is useful

for diagnosing susceptibility to diseases by detecting mutations in the

HPIA041 gene, and can diagnose diseases associated with HPIA041 protein

imbalance by determining HPIA041 polypeptide expression levels. Agonists and antagonists of the protein can be used in treatment to activate (agonist) or inhibit (antagonist) HPIA041 activity, in addition to direct administration of antitense sequences to prevent expression, or HPIA041 polynucleotides to treat conditions associated with a lack of HPIA041 protein. Gene therapy may also be used to affect endogenous HPIA041 polypeptide expression. HPIA041 antibodies are useful for inducing an immune response or purifying the polypeptide disease, and for isolating HPIA041 clones or purifying the polypeptides by affinity chromatography. HPIA041 polypeptides can be administered directly or as a vaccine to inoculate against disease. Diseases diagnosed, prevented and treated include bacterial, fungal, protozoan and viral infections, particularly HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcers; asthma; allergies; benign prostatic hypertrophy; and psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington's disease or Gilles de la Tourette's syndrome. The HPIA041 polypeptide is also useful for mapping the gene to a chromosome, allowing gene inheritance to be studied through linkage analysis

Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 8.8e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENENGTVDYSGYELICIKEDVREFAKVFLVFLTIVFVIGLAGNS 60
DB 1 MALEQNSTDYEEENENGTVDYSGYELICIKEDVREFAKVFLVFLTIVFVIGLAGNS 60
QY 61 MVAATAYAYKKKRTKDYIINLAVALDLLLFTLPFAVNAVHGWLGKIMCKITSALYT 120
DB 61 MVAATAYAYKKKRTKDYIINLAVALDLLLFTLPFAVNAVHGWLGKIMCKITSALYT 120
QY 121 INFVSGMQLACISIDRYAVAVTKVPSQSGVGKPCWNIICFVMAAILLSIPOLVFYVND 180
DB 121 INFVSGMQLACISIDRYAVAVTKVPSQSGVGKPCWNIICFVMAAILLSIPOLVFYVND 180
QY 181 NARCIPIFRYVIGTSMKALIQMLEICIGFVFPFLMGVCFITARTLMKMPNIKISRLK 240
DB 181 NARCIPIFRYVIGTSMKALIQMLEICIGFVFPFLMGVCFITARTLMKMPNIKISRLK 240
QY 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLLTSCMSKRMIDIAQVTSIALFHSCLNP 300
DB 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLLTSCMSKRMIDIAQVTSIALFHSCLNP 300
QY 301 ILVFMGASFKNYVMKVAKKYGSWROROSVEEFPDSEGPTEPTSTFSI 350
DB 301 ILVFMGASFKNYVMKVAKKYGSWROROSVEEFPDSEGPTEPTSTFSI 350

RESULT 2
AAV17435
ID AAV17435 standard; protein; 350 AA.

AAV17435;

29-JUN-1999 (first entry)

Human signal peptide-containing protein SP-16.

Human signal peptide-containing protein; SP; cell proliferation; cancer; neuronal disorder; immune response; detection.

Homo sapiens.

WO9924463-A2.

20-MAY-1999.

04-NOV-1998; 98WO-US023578.

07-NOV-1997; 97US-00966316.
(INCYTE) INCYTE PHARM INC.
Lai P, Au-Young J, Reddy R, Murty LB, Mathur P,
WPI; 1999-337694/28.
DR N-PSDB; AAX61288.
CDNA clones encoding signal peptide-containing proteins.
Claim 1; Fig 1; 83pp; English.
The present sequence represents a human signal peptide-containing protein (SP), designated SP-16. SP proteins can be used to stimulate cell proliferation or to treat or prevent cancer. SP antagonists are also used to treat or prevent cancer, and also for treating or preventing neuronal disorders or immune responses. Polynucleotide sequences complementary to the SP-encoding polynucleotides are useful for the detection of SP-encoding nucleic acid molecules in biological samples

Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 8.8e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENENGTVDYSGYELICIKEDVREFAKVFLVFLTIVFVIGLAGNS 60
DB 1 MALEQNSTDYEEENENGTVDYSGYELICIKEDVREFAKVFLVFLTIVFVIGLAGNS 60
QY 61 MVAATAYAYKKKRTKDYIINLAVALDLLLFTLPFAVNAVHGWLGKIMCKITSALYT 120
DB 61 MVAATAYAYKKKRTKDYIINLAVALDLLLFTLPFAVNAVHGWLGKIMCKITSALYT 120
QY 121 INFVSGMQLACISIDRYAVAVTKVPSQSGVGKPCWNIICFVMAAILLSIPOLVFYVND 180
DB 121 INFVSGMQLACISIDRYAVAVTKVPSQSGVGKPCWNIICFVMAAILLSIPOLVFYVND 180
QY 181 NARCIPIFRYVIGTSMKALIQMLEICIGFVFPFLMGVCFITARTLMKMPNIKISRLK 240
DB 181 NARCIPIFRYVIGTSMKALIQMLEICIGFVFPFLMGVCFITARTLMKMPNIKISRLK 240
QY 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLLTSCMSKRMIDIAQVTSIALFHSCLNP 300
DB 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLLTSCMSKRMIDIAQVTSIALFHSCLNP 300
QY 301 ILVFMGASFKNYVMKVAKKYGSWROROSVEEFPDSEGPTEPTSTFSI 350
DB 301 ILVFMGASFKNYVMKVAKKYGSWROROSVEEFPDSEGPTEPTSTFSI 350

RESULT 3
AAV57290
ID AAV57290 standard; protein; 350 AA.

AAV57290;

05-JUN-2000 (first entry)

Human BGCKr protein.

BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis; cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV; anti-allergic; antiviral.

Homo sapiens.

WO9952945-A2.

21-OCT-1999.

Query Match	100.0%	Score 1819	DB 2	Length 350
Best Local Similarity	100.0%	Pred. No. 8-195		
Matches 350	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MALEONQSTDYVYENENNGIYDSQYELICIKEDVREFAKYLEPVLITVFVIGLAGNS	60	
Db	1	MALEONQSTDYVYENENNGIYDSQYELICIKEDVREFAKYLEPVLITVFVIGLAGNS	60	
QY	61	MVVAIAVAYKKORTEDVYIINLAADLLIPTLPFMAVNAVHGWLGKIMCKITSALYT	120	
Db	61	MVVAIAVAYKKORTEDVYIINLAADLLIPTLPFMAVNAVHGWLGKIMCKITSALYT	120	
QY	121	LNFSVGMQFLACISIDRYVAVATKVPSQSGVGRKPCWIIICPCVMAAILLSIPOLVETVND	180	
Db	121	LNFSVGMQFLACISIDRYVAVATKVPSQSGVGRKPCWIIICPCVMAAILLSIPOLVETVND	180	
QY	181	NARCPITPRYIGTSMKALIQMLELFCIGVAVFFILMGVGYEFTTARTIMKMPIKISRPKX	240	
Db	181	NARCPITPRYIGTSMKALIQMLELFCIGVAVFFILMGVGYEFTTARTIMKMPIKISRPKX	240	
QY	241	VLLTVAVIFVITQLPEYNIKFCRAIDIIISLTSCNMSKRMIDIAIQVTSIALPFSCLNP	300	
Db	241	VLLTVAVIFVITQLPEYNIKFCRAIDIIISLTSCNMSKRMIDIAIQVTSIALPFSCLNP	300	
QY	301	ILYVFMGASFKNYVMKVAKKYGSWRQPSVEFPDSDGPEPSTFSI	350	
Db	301	ILYVFMGASFKNYVMKVAKKYGSWRQPSVEFPDSDGPEPSTFSI	350	
RESULT 4				
AAV94325				
ID	AAV94325 standard; protein; 350 AA.			
XX	AAV94325;			
XX	11-AUG-2000 (first entry)			
XX	Human seven transmembrane receptor VSHK-1.			
XX	Human, seven transmembrane receptor; VSHK-1; signal transduction.			

XX	Homo sapiens.	Location/Qualifiers
XX	Key	6. .8
FT	Modified-site	/note= "potential N-glycosylation site"
FT	Modified-site	19. .21
FT	Modified-site	/note= "potential N-glycosylation site"
FT	Domain	42. .66
FT	Domain	/label= Transmembrane_domain
FT	Domain	79. .100
FT	Domain	/label= Transmembrane_domain
FT	Domain	114. .135
FT	Domain	/label= Transmembrane_domain
FT	Domain	156. .175
FT	Domain	/label= Transmembrane_domain
FT	Domain	199. .221
FT	Domain	/label= Transmembrane_domain
FT	Domain	241. .262
FT	Domain	/label= Transmembrane_domain
FT	Modified-site	276. .278
FT	Modified-site	/note= "potential N-glycosylation site"
FT	Domain	287. .308
FT	Domain	/label= Transmembrane_domain
XX	WO200026369-A1.	
XX	11-MAY-2000.	
XX	03-NOV-1999.	99WO-US025848.
XX	04-NOV-1998.	98US-0107112P.
XX	06-JAN-1999.	99US-0114856P.
XX	(CHIR) CHIRON CORP.	
XX	XhoIa H, Shymala V;	
XX	WPI, 2000-365618/31.	
XX	N-PSDB; AA943325.	
XX	Novel polypeptide comprising a new seven-transmembrane receptor protein and its encoding polynucleotide, useful for the analysis of VSHK-1.	
XX	Claim 3; Fig 1; 79pp; English.	
XX	The present sequence is VSHK-1, a new seven transmembrane receptor which contains seven membrane-spanning helical domains that are linked by three intracellular and three extracellular loops. The gene sequence encoding VSHK-1 was isolated from a cDNA library. In heart tissue, where VSHK-1 is predominantly found, three RNA species were identified: a 1.3kb; a 2.0kb; and a 5.0kb species. The polynucleotide encoding the present sequence corresponds to the 2.0kb form. The 1.3kb form may result from the use of an alternative polyadenylation site while transcription of a 3.0kb intron at nucleotide 74 could account for the 5.0kb species. VSHK-1 polynucleotides can be used as hybridisation probes to detect and measure VSHK-1 mRNA. They may also be used to identify substances that modulate the level of VSHK-1 mRNA. The VSHK-1 coding sequence can be integrated into an expression vector for production of VSHK-1 receptor polypeptides in host cells. The polypeptides can be used to identify agents which modulate VSHK-1 receptor signal transduction activity	
XX	Sequence 350 AA;	
XX	Query Match	100.0%; Score 1819; DB 3; Length 350;
XX	Best Local Similarity	100.0%; Pred. No. 8.8e-195;
XX	Matches 350; Conservative	0; Mismatches 0; Indels 0; Gaps 0
XX	1 MALEONOSDYDYENENMGATDYSQVYLICIKEDVAPKAVLPVPLTIVFVIGLAGNS 60	
XX	1 MALEONOSDYDYENENMGATDYSQVYLICIKEDVAPKAVLPVPLTIVFVIGLAGNS 60	
XX	61 MVAIAIYAYKORIKTDYIILNVAADILLFTLPMAVNAHGVULGIKMCITISALT 120	

Db 61 MVVAIYAYKKORTDVIYIIINLAVADLLFTLPFMAVNAVHGVLGKIMCKITSALYT 120

QY 121 LNFVSGMOFLACISIDRYVAATKVPSSQGVGKPCMIICFCVMAAILLSIQLVFTYND 180

Db 121 LNFVSGMOFLACISIDRYVAATKVPSSQGVGKPCMIICFCVMAAILLSIQLVFTYND 180

QY 181 NARCIPFPRLYIGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNKRISRLK 240

Db 181 NARCIPFPRLYIGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNKRISRLK 240

QY 241 VLLTVVIVFIVTQLPYNTVKEFCRAIDIIYSLSITSCMSKMDIAIQVTSIALFHSCLNP 300

Db 241 VLLTVVIVFIVTQLPYNTVKEFCRAIDIIYSLSITSCMSKMDIAIQVTSIALFHSCLNP 300

QY 301 ILVYFMGASFKNYVMKVAKKYGSWRQROQSVYEEFPDSEGPTEPTSTFSI 350

Db 301 ILVYFMGASFKNYVMKVAKKYGSWRQROQSVYEEFPDSEGPTEPTSTFSI 350

RESULT 5

AAU08994

ID AAU08994 standard; protein; 350 AA.

AC AAU08994;

XX

DT 18-DEC-2001 (first entry)

DE Human G protein-coupled receptor, GPCR, 2398.

XX

KM Human; GPCR; G protein-coupled receptor; 2398; cardiac; antiatherosclerotic; analgesic; cytotactic; antiangiogenic; cardiovascular disorder; angiogenesis-related disorder; neural disorder; pain response disorder; inflammatory disorder; atherosclerosis; angina pectoris; myocardial infarction; ischaemic heart disease; sudden cardiac death; obesity; hypertensive heart disease; diabetes; prostate cancer-related pain.

KM

XX

OS Homo sapiens.

XX

Key Location/Qualifiers

FT Region 125..141

FT /label=G_protein_receptor_signature

XX

XX WO200164882-A2.

XX

XX 07-SEP-2001.

XX

XX 28-FEB-2001; 2001MO-US006543.

XX

XX 29-FEB-2000; 2000US-0186059P.

XX

XX (MILL-) MILLENNIUM PHARM INC.

XX

XX Glucksmann MA, Galvin KM, Silos-Santiago I;

XX

XX WPI, 2001-589866/66.

XX

XX N-PSDB; AAS14572.

XX

XX Novel G protein coupled receptors and nucleic acids encoding them, for identifying agents for the treatment of cardiac disorders.

XX

XX Claim 9; Fig 9; 209pp; English.

XX

XX The invention relates to novel human G protein-coupled receptors (GPCR) named 1983, 52881, 2398, 45449, 50289 and 52872. The novel GPCRs and nucleic acids encoding them are useful for identifying agents for the treatment of cardiovascular disorders, angiogenesis-related disorders, neural disorders, pain response disorders and inflammatory disorders e.g. atherosclerosis, angina pectoris and myocardial infarction, ischaemic heart disease, sudden cardiac death, hypertensive heart disease, diabetes, prostate cancer-related pain, diabetes and obesity. The present sequence represents GPCR 2398

Seq Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 4; Length 350;

Best Local Similarity 100.0%; Pred. No. 8.8e-195;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEONOSTDYEEENENNGYDYSQVELLICKEDVEFEAVFLPVELTIVFVGLAGNS 60

Db 1 MLEONOSTDYEEENENNGYDYSQVELLICKEDVEFEAVFLPVELTIVFVGLAGNS 60

QY 61 MVVAIYAYKKORTDVIYIIINLAVADLLFTLPFMAVNAVHGVLGKIMCKITSALYT 120

Db 61 MVVAIYAYKKORTDVIYIIINLAVADLLFTLPFMAVNAVHGVLGKIMCKITSALYT 120

QY 121 LNFVSGMOFLACISIDRYVAATKVPSSQGVGKPCMIICFCVMAAILLSIQLVFTYND 180

Db 121 LNFVSGMOFLACISIDRYVAATKVPSSQGVGKPCMIICFCVMAAILLSIQLVFTYND 180

QY 181 NARCIPFPRLYIGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNKRISRLK 240

Db 181 NARCIPFPRLYIGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNKRISRLK 240

QY 241 VLLTVVIVFIVTQLPYNTVKEFCRAIDIIYSLSITSCMSKMDIAIQVTSIALFHSCLNP 300

Db 241 VLLTVVIVFIVTQLPYNTVKEFCRAIDIIYSLSITSCMSKMDIAIQVTSIALFHSCLNP 300

QY 301 ILVYFMGASFKNYVMKVAKKYGSWRQROQSVYEEFPDSEGPTEPTSTFSI 350

Db 301 ILVYFMGASFKNYVMKVAKKYGSWRQROQSVYEEFPDSEGPTEPTSTFSI 350

RESULT 6

AAG80119

ID AAG80119 standard; protein; 350 AA.

AC AAG80119;

XX

DT 17-JAN-2002 (first entry)

DE Human CCR11 protein.

XX

KM Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytotoxic; antiinflammatory; antiaesthetic; immunosuppressive; dermatological; antineumatic; antidiabetic.

KM

XX

OS Homo sapiens.

XX

XX WO200172830-A2.

XX

XX 04-OCT-2001.

XX

XX 02-APR-2001; 2001MO-EP003708.

XX

XX 31-MAR-2000; 2000DE-01016013.

XX

XX (TFP-) TFP PHARM GMBH.

XX

XX (FORS/) FORSMANN U.

XX

XX Forssmann W, Adernann K, Heitland A, Spodberg N;

XX

XX WPI, 2001-626256/72.

XX

XX Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors.

XX

XX Disclosure; Page 11; 26pp; German.

XX

XX This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal

CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (1) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antiaesthetic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80945-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention

XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 4; Length 350;
 Best Local Similarity 100.0%; Pred. No. 8.8e-195;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENNGTIDYQYELICKEVDREPAKVFLEPLTIVFVIGLAGNS 60
 DB 1 MALEQNSTDYEEENNGTIDYQYELICKEVDREPAKVFLEPLTIVFVIGLAGNS 60
 QY 61 MVAIAIYAYKKQRTKDVYILNLAVALDLLFTLPFWANAVHGWLGKIMCKITSALT 120
 DB 61 MVAIAIYAYKKQRTKDVYILNLAVALDLLFTLPFWANAVHGWLGKIMCKITSALT 120
 QY 121 INFVSGMGFLACISIDRYAVATKVPQSQGVKPCWIIICFWMAAILLSIPOLVFTYND 180
 DB 121 INFVSGMGFLACISIDRYAVATKVPQSQGVKPCWIIICFWMAAILLSIPOLVFTYND 180
 QY 181 NARCIPIPRRYGTSMKALIQMLEICIGFVVPFLMGVCYFTATLMKMPKISRLK 240
 DB 181 NARCIPIPRRYGTSMKALIQMLEICIGFVVPFLMGVCYFTATLMKMPKISRLK 240
 QY 241 VLTIVVIFIVTQLPNIVKFCRAIDIIYSLITSQMSKMDIAIOVTESIALFHSCLNP 300
 DB 241 VLTIVVIFIVTQLPNIVKFCRAIDIIYSLITSQMSKMDIAIOVTESIALFHSCLNP 300
 QY 301 ILVYFMGASFKNYVMKVAKKYGSRRQROSVVEFPDSEGPTEPTSTSI 350
 DB 301 ILVYFMGASFKNYVMKVAKKYGSRRQROSVVEFPDSEGPTEPTSTSI 350

RESULT 7
 AAG67237

ID AAG67237 standard; protein; 350 AA.

AC AAG67237;

DT 13-NOV-2001 (first entry)

DE Amino acid sequence of human chemokine receptor CCR11.

XX Human; chemokine receptor; CCR11; G protein coupled receptor;
 XX inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;
 XX asthma; angiogenesis; atherosclerosis vascular association disease;
 XX hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;
 XX left ventricular diastolic dysfunction; migraine; preterm labour;
 XX oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;
 XX myocardial infarction; congestive heart failure; endometritis;
 XX vasospasm; retinopathy; nephropathy; pulmonary vascular disease.

OS Homo sapiens.

PN MO200166598-A2.

PD 13-SEP-2001.

PF 05-MAR-2001; 2001WO-US007073.

PR 03-MAR-2000; 2000US-0186928P.

PR 03-MAR-2000; 2000US-0187231P.

XX (ICOS-1) ICOS CORP.

PI Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;

XX WPI; 2001-541918/60.

DR N-PSDB; AAH77711.

PT An isolated polynucleotide encoding the chemokine receptor CCR11, useful
 PT for treating rheumatoid arthritis, inflammatory bowel disease, asthma,
 PT angiogenesis, atherosclerosis, cardiac arrhythmias, Raynaud's phenomenon
 PT and migraine.

XX Claim 13; Page 96-97; 110pp; English.

XX The present sequence represents the human chemokine receptor CCR11. CCR11
 CC is a member of the G protein coupled receptor family. A CCR11
 CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11
 CC expression or biological activity, is useful for treating many
 CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory
 CC bowel disease, and asthma. They are also useful for treating
 CC angiogenesis, atherosclerosis vascular association diseases which may
 CC include but are not limited to hypertension, angina pectoris, cardiac
 CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's
 CC phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic
 CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive heart
 CC failure, endometritis, vasospasm, retinopathy, nephropathy, or pulmonary
 CC vascular disease

XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 4; Length 350;
 Best Local Similarity 100.0%; Pred. No. 8.8e-195;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENNGTIDYQYELICKEVDREPAKVFLEPLTIVFVIGLAGNS 60
 DB 1 MALEQNSTDYEEENNGTIDYQYELICKEVDREPAKVFLEPLTIVFVIGLAGNS 60
 QY 61 MVAIAIYAYKKQRTKDVYILNLAVALDLLFTLPFWANAVHGWLGKIMCKITSALT 120
 DB 61 MVAIAIYAYKKQRTKDVYILNLAVALDLLFTLPFWANAVHGWLGKIMCKITSALT 120
 QY 121 INFVSGMGFLACISIDRYAVATKVPQSQGVKPCWIIICFWMAAILLSIPOLVFTYND 180
 DB 121 INFVSGMGFLACISIDRYAVATKVPQSQGVKPCWIIICFWMAAILLSIPOLVFTYND 180
 QY 181 NARCIPIPRRYGTSMKALIQMLEICIGFVVPFLMGVCYFTATLMKMPKISRLK 240
 DB 181 NARCIPIPRRYGTSMKALIQMLEICIGFVVPFLMGVCYFTATLMKMPKISRLK 240
 QY 241 VLTIVVIFIVTQLPNIVKFCRAIDIIYSLITSQMSKMDIAIOVTESIALFHSCLNP 300
 DB 241 VLTIVVIFIVTQLPNIVKFCRAIDIIYSLITSQMSKMDIAIOVTESIALFHSCLNP 300
 QY 301 ILVYFMGASFKNYVMKVAKKYGSRRQROSVVEFPDSEGPTEPTSTSI 350
 DB 301 ILVYFMGASFKNYVMKVAKKYGSRRQROSVVEFPDSEGPTEPTSTSI 350

RESULT 8
 AAE37348

ID AAE37348 standard; protein; 350 AA.

AC AAE37348;

DT 27-AUG-2003 (first entry)

DE Human C-C chemokine receptor type 11 (CC CKR-11), 2398 protein.

XX Human; cardiovascular disorder; coronary artery disease; bradycardia;
 KW restenosis; cardiac hypertrophy; ischaemia reperfusion injury; angina;

arteriosclerosis; coronary artery ligation; rheumatic heart disease; heart failure; hypertension; cardiomyopathy; myocardial infarction; arterial inflammation; microembolism; atherosclerosis; endocarditis; vascular heart disease; valvular disease; arrhythmia; gene therapy; sinus node dysfunction; C-C chemokine receptor type 11; CC CKR-11; receptor.

XX Homo sapiens.

OS

XX MO2003039341-A2.

XX

XX 15-MAY-2003.

XX

XX 05-NOV-2002; 2002MO-US035538.

XX

XX 05-NOV-2001; 2001US-0339582P.

XX (MILL-) MILLENNIUM PHARM INC.

XX

XX Logan TJ, Chun M, Galvin KM;

XX

XX WPI: 2003-44137/41.

XX DR N-PSDB; AAD56515.

XX

XX Treating a subject having a cardiovascular disorder, e.g. angina, PT arrhythmia, or restenosis, comprises administering a 139, 258, 1261, PT 1486, 2398, 2414, 7660, 8587, 10183, 10550, 12680, 17921, 32248, 60489 or PT 93804 modulator.

XX

XX Disclosure; Page 105-106; 124pp; English.

XX

XX The invention relates to methods and compositions for treating a subject CC having a cardiovascular disorder using 139, 258, 1261, 1486, 2398, 2414, CC 7660, 8587, 10183, 10550, 12680, 17921, 32248, 60489 or 93804 modulator. CC The invention is useful for treating a cardiovascular disorder, including CC arteriosclerosis, atherosclerosis, vascular wall remodeling, restenosis, CC cardiac hypertrophy, ischemia reperfusion injury, arterial inflammation, CC ventricular remodeling, rapid ventricular pacing, tachycardia, coronary CC microembolism, bradycardia, pressure overload, aortic bending, coronary CC artery ligation, vascular heart disease, valvular disease, including but CC not limited to, valvular degeneration caused by calcification, rheumatic CC heart disease, endocarditis, or complications of artificial valves; CC atrial fibrillation, long-QT syndrome, congestive heart failure, sinus CC node dysfunction, angina, heart failure, hypertension, atrial flutter, CC atrial fibrillation, pericardial disease, including but not limited to CC pericardial effusion and pericarditis, cardiomyopathies (e.g. dilated CC cardiomyopathy or idiopathic cardiomyopathy), myocardial infarction, CC coronary artery disease, coronary artery spasm, ischemic disease, CC arrhythmia, sudden cardiac death, and cardiovascular developmental CC disorders. The invention is also useful in gene therapy. The present CC sequence is human C-C chemokine receptor type 11 (CC CKR-11) protein. CC This sequence is used to illustrate the method of the invention

XX

XX Sequence 350 AA;

XX

XX Query Match 100.0%; Score 1819; DB 6; Length 350;

XX Best Local Similarity 100.0%; Pred. No. 8.8e-195;

XX Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

XX 1 MALEONOSDYDYENENNGTGYDYOELICKEDEPFAKVPVPLTFIVFGIAGNS 60

XX 1 MALEONOSDYDYENENNGTGYDYOELICKEDEPFAKVPVPLTFIVFGIAGNS 60

XX 1 MALEONOSDYDYENENNGTGYDYOELICKEDEPFAKVPVPLTFIVFGIAGNS 60

XX 61 MVAAYAYKKORTKTDVYIINLAVADLLFTLPFMAVNAVGVGKIVCKITSAIYT 120

XX 61 MVAAYAYKKORTKTDVYIINLAVADLLFTLPFMAVNAVGVGKIVCKITSAIYT 120

XX 61 MVAAYAYKKORTKTDVYIINLAVADLLFTLPFMAVNAVGVGKIVCKITSAIYT 120

XX 121 LNFVSGMOPLACISIDRYAVAVKVPSSGVKPCIIICPCWMAAILISIQVLYTND 180

XX 121 LNFVSGMOPLACISIDRYAVAVKVPSSGVKPCIIICPCWMAAILISIQVLYTND 180

XX 121 LNFVSGMOPLACISIDRYAVAVKVPSSGVKPCIIICPCWMAAILISIQVLYTND 180

XX 181 NARCIPIFRYVGTSMKALIQMLEICIGFVVPFLIMGVCFYFTARTLMKMNKISRLK 240

DB 181 NARCIPIFRYVGTSMKALIQMLEICIGFVVPFLIMGVCFYFTARTLMKMNKISRLK 240

QY 241 VLLTVVIVFTVLTQLPYNIYKFCRAIDIIYSILTSQNSKRMIDIAQVETSLAFHSCINP 300

DB 241 VLLTVVIVFTVLTQLPYNIYKFCRAIDIIYSILTSQNSKRMIDIAQVETSLAFHSCINP 300

QY 301 ILVFMGASFKNYVMKAKKYSMROROSVSEPFDESGPEPTSTSI 350

DB 301 ILVFMGASFKNYVMKAKKYSMROROSVSEPFDESGPEPTSTSI 350

XX

XX RESULT 9

XX ABP81716

XX ID ABP81716 standard; protein; 350 AA.

XX

XX AC ABP81716;

XX

XX DT 04-MAR-2003 (first entry)

XX

XX DE Human C-C chemokine receptor 11 protein SEQ ID NO:607.

XX

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

XX G protein-coupled receptor modulator; antibody; immune-related disease;

XX growth-related disease; cell regeneration-related disease; AIDS; cancer;

XX immunological-related cell proliferative disease; autoimmune disease;

XX Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;

XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;

XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

XX hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

XX ulcer.

XX

XX OS Homo sapiens.

XX

XX MO200261087-A2.

XX

XX 08-AUG-2002.

XX

XX 19-DEC-2001; 2001MO-US050107.

XX

XX 19-DEC-2000; 2000US-0257144P.

XX

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX

XX Burner GC, Roush CL, Brown JP;

XX

XX WPI: 2003-046718/04.

XX

XX N-PSDB; ABZ42562.

XX

XX New isolated antigenic peptides e.g., for G protein-coupled receptors

XX (GPCR), useful for diagnosing and designing drugs for treating conditions

XX PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or

XX PT autoimmune diseases.

XX

XX PS Disclosure; Fig 1; 523pp; English.

XX

XX The present invention describes antigenic peptides (I) comprising: (a)

XX CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino

XX CC acids. Also described: (1) an assay for the detection of a particular G

XX CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;

XX CC and (2) an isolated antibody having high specificity and high affinity or

XX CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in

XX CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an

XX CC antibody against a particular GPCR, and in the production of specific

XX CC antibodies. The peptides and antibodies are also useful for detecting the

XX CC presence or absence of corresponding GPCRs. The antigenic peptides for

XX CC GPCR and antibodies are useful for diagnosing and designing drugs for

XX CC treating immune-related diseases, growth-related diseases, cell

XX CC regeneration-related disease, immunological-related cell proliferative

XX CC disease, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,

XX CC atherosclerosis, bacterial, fungal, protozoan or viral infections,

XX CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute

CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242669 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention

XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 6; Length 350;
 Best Local Similarity 100.0%; Pred. No. 8.8e-195;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENENNGTYDSQYELICTKEDVREFAKVLPVFLTIVFVIGLAGNS 60
 DB 1 MALEQNSTDYEEENENNGTYDSQYELICTKEDVREFAKVLPVFLTIVFVIGLAGNS 60
 QY 61 MVAATYAYKKKRTKTDVYILNLAVADLLFLTPFMAVNAVHGWLGKIMCKITSALYT 120
 DB 61 MVAATYAYKKKRTKTDVYILNLAVADLLFLTPFMAVNAVHGWLGKIMCKITSALYT 120
 QY 121 LNFVSGMQFLACISIDRYVAATKVPSSQGVGKPCWIIICFCVMAAILLSIPOLVFTYVND 180
 DB 121 LNFVSGMQFLACISIDRYVAATKVPSSQGVGKPCWIIICFCVMAAILLSIPOLVFTYVND 180
 QY 181 NARCIPIPRVYIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKMPNIXISRPK 240
 DB 181 NARCIPIPRVYIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKMPNIXISRPK 240
 QY 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300
 DB 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300
 QY 301 ILVFMGASFKNYVMKAKYGSWRQROSVBEPPDSGPTPEPTSTFSI 350
 DB 301 ILVFMGASFKNYVMKAKYGSWRQROSVBEPPDSGPTPEPTSTFSI 350

RESULT 10

ID ADA10754 standard; protein; 350 AA.

AC ADA10754;

DT 06-NOV-2003 (first entry)

XX Human signal peptide, containing protein SP-16 Incyte 2547007.

DE human; signal peptide-containing protein; cell proliferation disorder;

KM cell signaling disorder; Huntington's disease; stomach cancer;

KM uterine cancer; mucinous cystadenoma; arthritis; testicular seminoma;

KM prostate cancer; bladder cancer; renal cell cancer; schizophrenia;

KM asthma; cancer;

XX Homo sapiens.

OS US2003073162-A1.

XX 17-APR-2003.

PF 01-OCT-2001; 2001US-00968433.

XX 07-NOV-1997; 97US-00966316.

PR 17-MAR-1999; 99US-00271110.

XX (LALP/) LAL P. G.

PA (AUTO/) AU-YOUNG J.

PA (REDD/) REDDY R.

PA (MURR/) MURRY L. E.

PA (MATH/) MATHUR P.

XX LAL P.G. Au-Young J, Reddy R, Murry LE, Mathur P;
 PI WPI; 2003-567307/53.
 XX N-PSDB; ADA10755.

PT New signal peptide-containing proteins and nucleic acids, useful in
 PT diagnosing, prognosing, treating or evaluating therapies for disorders
 PT associated with cell proliferation and cell signaling.

XX Claim 1; Fig 1; 59pp; English.

XX The invention relates to a new purified signal peptide-containing
 CC protein. The signal peptide-containing proteins and nucleic acids
 CC encoding them are useful in diagnosing, prognosing, treating or
 CC evaluating therapies for disorders associated with cell proliferation and
 CC cell signaling such as Huntington's disease, stomach cancer, uterine
 CC cancer, mucinous cystadenoma, arthritis, testicular seminoma, prostate
 CC cancer, bladder cancer, renal cell cancer, schizophrenia, asthma and
 CC cancer. The nucleic acids may be used in hybridisation, amplification and
 CC screening technologies to identify and distinguish among the identical
 CC and related molecules in a sample and to produce transgenic cell lines or
 CC organisms which are model systems for cancers and upon which the toxicity
 CC and efficacy of potential therapeutic treatments may be tested. The
 CC present sequence represents the amino acid sequence of a human signal
 CC peptide containing protein.

XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 7; Length 350;
 Best Local Similarity 100.0%; Pred. No. 8.8e-195;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENENNGTYDSQYELICTKEDVREFAKVLPVFLTIVFVIGLAGNS 60
 DB 1 MALEQNSTDYEEENENNGTYDSQYELICTKEDVREFAKVLPVFLTIVFVIGLAGNS 60
 QY 61 MVAATYAYKKKRTKTDVYILNLAVADLLFLTPFMAVNAVHGWLGKIMCKITSALYT 120
 DB 61 MVAATYAYKKKRTKTDVYILNLAVADLLFLTPFMAVNAVHGWLGKIMCKITSALYT 120
 QY 121 LNFVSGMQFLACISIDRYVAATKVPSSQGVGKPCWIIICFCVMAAILLSIPOLVFTYVND 180
 DB 121 LNFVSGMQFLACISIDRYVAATKVPSSQGVGKPCWIIICFCVMAAILLSIPOLVFTYVND 180
 QY 181 NARCIPIPRVYIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKMPNIXISRPK 240
 DB 181 NARCIPIPRVYIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKMPNIXISRPK 240
 QY 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300
 DB 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300
 QY 301 ILVFMGASFKNYVMKAKYGSWRQROSVBEPPDSGPTPEPTSTFSI 350
 DB 301 ILVFMGASFKNYVMKAKYGSWRQROSVBEPPDSGPTPEPTSTFSI 350

RESULT 11

ID AAB62389 standard; protein; 382 AA.

XX AAB62389;

DT 29-JUN-2001 (first entry)

XX Human chemokine receptor CCX CKR polypeptide.

DE Chemokine receptor; CCX CKR; chemokine; ELC; SLG; TECK; modulator;

KM antiinflammatory; immunosuppressive; cytostatic; antiallergic; human;

XX Immunostimulant; gene therapy.

OS Homo sapiens.

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XX Key Location/Qualifiers
FH MISC-difference 351
FT /note= "encoded by TAA"
FT MISC-difference 353
FT /note= "encoded by TAA"
FT MISC-difference 365
FT /note= "encoded by TAA"
FT MISC-difference 371
FT /note= "encoded by TAA"
XX W0200127146-A2.
XX 19-APR-2001.
XX 10-OCT-2000; 2000WO-US028067.
XX 12-OCT-1999; 99US-0159015P.
XX 13-OCT-1999; 99US-0159210P.
XX 20-DEC-1999; 99US-0172979P.
XX 28-DEC-1999; 99US-0173388P.
XX 03-MAR-2000; 2000US-018662EP.
XX (CHEM-) CHEMOCENTRIX INC.
XX Goelings J, Dairaghi DJ, Hanley M, Miao Z, Talbot D, Schall TJ;
XX WPI; 2001-281975/29.
XX N-PSDB; AAF57685.
XX Isolated or recombinant chemokine receptor (designated CCX CR)
XX polypeptide (P1) or its fragment, useful for identifying CCX CR
XX modulators which can be used in the treatment of inflammation, allergy,
XX an autoimmune disease or cancer.
XX Claim 4; Fig 1; 72pp; English.
XX The invention relates to an isolated or recombinant chemokine receptor
XX designated CCX CR) polypeptide which binds to chemokines such as ELC,
XX SLK or TREM. The CCX CR polypeptide is useful for identifying CCX CR
XX modulators. An agent that modulates the activity or expression of CCX CR
XX in a cell or tissue in the mammal is useful in the treatment of a CCX CR
XX mediated condition such as inflammation, allergy, an autoimmune disease,
XX graft rejection, cancer, an infectious disease or an immunosuppressive
XX disease. The present sequence represents the human CCX CR polypeptide
XX sequence 382 AA;
SQ
Query Match 100.0%; Score 1819; DB 4; Length 382;
Best Local Similarity 100.0%; Pred. No. 9.8e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MALEONOSTDYVEENENAGTYDYSEYELICIKEDVEFAKVPFLVFLVIVGVLGAGNS 60
1 MALEONOSTDYVEENENAGTYDYSEYELICIKEDVEFAKVPFLVFLVIVGVLGAGNS 60
1 MALEONOSTDYVEENENAGTYDYSEYELICIKEDVEFAKVPFLVFLVIVGVLGAGNS 60
61 MVAIAYAYKKQRTDYIINLAVADLLIFLPMAVNAHGVLGKIMCKITSLALT 120
61 MVAIAYAYKKQRTDYIINLAVADLLIFLPMAVNAHGVLGKIMCKITSLALT 120
61 MVAIAYAYKKQRTDYIINLAVADLLIFLPMAVNAHGVLGKIMCKITSLALT 120
61 MVAIAYAYKKQRTDYIINLAVADLLIFLPMAVNAHGVLGKIMCKITSLALT 120
121 LNFSWGMFLACISIDRYAVATKVPSSGVGKPCMTICFCVMAAILLSIPOLVFTVND 180
121 LNFSWGMFLACISIDRYAVATKVPSSGVGKPCMTICFCVMAAILLSIPOLVFTVND 180
121 LNFSWGMFLACISIDRYAVATKVPSSGVGKPCMTICFCVMAAILLSIPOLVFTVND 180
121 LNFSWGMFLACISIDRYAVATKVPSSGVGKPCMTICFCVMAAILLSIPOLVFTVND 180
181 NARCIPIPRYLGSMKALIMLEICIGFVVPFLIMGVCFITARTMKMKNIKISPLK 240
181 NARCIPIPRYLGSMKALIMLEICIGFVVPFLIMGVCFITARTMKMKNIKISPLK 240
181 NARCIPIPRYLGSMKALIMLEICIGFVVPFLIMGVCFITARTMKMKNIKISPLK 240
181 NARCIPIPRYLGSMKALIMLEICIGFVVPFLIMGVCFITARTMKMKNIKISPLK 240
241 VLTAVIVFIVTQPYNVKRCRAIDILYSITSONSKRMDIAIQTESIALFHSCLNP 300
241 VLTAVIVFIVTQPYNVKRCRAIDILYSITSONSKRMDIAIQTESIALFHSCLNP 300
241 VLTAVIVFIVTQPYNVKRCRAIDILYSITSONSKRMDIAIQTESIALFHSCLNP 300
241 VLTAVIVFIVTQPYNVKRCRAIDILYSITSONSKRMDIAIQTESIALFHSCLNP 300
301 ILVFMGASPKXNYVMKAKYGSWRKQSVSEFPSEGPTEPTSTFSI 350
301 ILVFMGASPKXNYVMKAKYGSWRKQSVSEFPSEGPTEPTSTFSI 350

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DB 301 ILVFMGASPKXNYVMKAKYGSWRKQSVSEFPSEGPTEPTSTFSI 350
RESULT 12
ID AAM931170
ID AAM931170 standard; protein; 349 AA.
XX AAM931170;
XX 24-MAY-1999 (first entry)
XX Human HPIAO41 protein.
XX HPIAO41, G-coupled receptor; disease susceptibility; diagnosis; immunise;
XX treatment; HPIAO41 protein; gene therapy; immune response; vaccine; HIV-2;
XX inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;
XX diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;
XX hypertension; hypertension; urinary retention; osteoporosis; allergy;
XX benign prostatic hyperplasia; myocardial infarction; ulcer; asthma; schizophrenia;
XX anxiety; manic depression; delirium; dementia; severe mental retardation;
XX dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;
XX linkage analysis; gene mapping; human; ss.
XX Homo sapiens.
XX EP899332-A2.
XX 03-MAR-1999.
XX 17-FEB-1998; 98EP-00301170.
XX 15-AUG-1997; 97US-0055895P.
XX 27-OCT-1997; 97US-00962922.
XX (SMK) SMITHKLINE BEECHAM CORP.
XX Ellis CE;
XX WPI; 1999-144803/13.
XX N-PSDB; AAX22558.
XX New G-coupled receptor (HPIAO41) polypeptide and polynucleotide - useful
XX as diagnostic reagents and for prevention and treatment of cancer, HIV
XX infections and Parkinson's disease.
XX Disclosure; Page 25-26; 27pp; English.
XX This sequence encodes a G-coupled receptor, HPIAO41 which is useful for
XX diagnosing susceptibility to diseases by detecting mutations in the
XX HPIAO41 gene, and can diagnose diseases associated with HPIAO41 protein
XX imbalance by determining HPIAO41 polypeptide expression levels. Agonists
XX and antagonists of the protein can be used in treatment to activate
XX (agonist) or inhibit (antagonist) HPIAO41 activity. In addition to direct
XX administration of antisense sequences to prevent expression, or HPIAO41
XX polynucleotides to treat conditions associated with a lack of HPIAO41
XX protein. Gene therapy may also be used to affect endogenous HPIAO41
XX polypeptide expression. HPIAO41 antibodies are useful for inducing an
XX immune response to immunise and prevent disease, and for isolating
XX HPIAO41 clones or purifying the polypeptides by affinity chromatography.
XX HPIAO41 polypeptides can be administered directly or as a vaccine to
XX inoculate against disease. Diseases diagnosed, prevented and treated
XX include bacterial, fungal, protozoan and viral infections, particularly
XX HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's
XX disease; acute heart failure; hypertension; hypertension; urinary
XX retention; osteoporosis; benign prostatic hyperplasia; myocardial infarction;
XX asthma; allergies; benign prostatic hyperplasia; and psychotic and
XX neurological disorders, including anxiety, schizophrenia, manic
XX depression, delirium, dementia, severe mental retardation and dyskinesias
XX such as Huntington's disease or Gilles de la Tourette's syndrome. The
XX HPIAO41 polypeptide is also useful for mapping the gene to a chromosome,
XX allowing gene inheritance to be studied through linkage analysis

```


XX SQ Sequence 349 AA;
 Query Match 99.7%; Score 1814; DB 2; Length 349;
 Best Local Similarity 100.0%; Pred. No. 3,2e-194;
 Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ALEONQSTDYEEENNGTYDYSQYELICKEVDREFAKFLPVFLTVFVIGLAGNSM 61
 DB 1 ALEONQSTDYEEENNGTYDYSQYELICKEVDREFAKFLPVFLTVFVIGLAGNSM 60
 QY 62 VVAIAIYKQKRTKDVIILMLAVADLLFLTFPMWANAAGWLGKIMKITSALYT 121
 DB 61 VVAIAIYKQKRTKDVIILMLAVADLLFLTFPMWANAAGWLGKIMKITSALYT 120
 QY 122 NFVSGMOFLACISIDRYAVATKVPQSGVGKPCWIIICCVMAAILLSIPOLVFTVND 181
 DB 121 NFVSGMOFLACISIDRYAVATKVPQSGVGKPCWIIICCVMAAILLSIPOLVFTVND 180
 QY 182 ARCTIFPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNIXSRPLK 241
 DB 181 ARCTIFPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNIXSRPLK 240
 QY 242 LLTVVIVFIVTQLPYNIVKFCRAIDIIYSLTSCNMSKRMIDIAIQVTESIALFHSCLNP 301
 DB 241 LLTVVIVFIVTQLPYNIVKFCRAIDIIYSLTSCNMSKRMIDIAIQVTESIALFHSCLNP 300
 QY 302 LYVFMGASFKNYVMKVAKKYGSWRQROSVBEPDSEGPTEPTSTFSI 350
 DB 301 LYVFMGASFKNYVMKVAKKYGSWRQROSVBEPDSEGPTEPTSTFSI 349

RESULT 13
 ID AAY30125
 AC AAY30125 standard; protein; 350 AA.
 XX AAY30125;
 XX
 DT 14-OCT-1999 (first entry)
 DE A human seven-pass transmembrane receptor protein.
 XX
 KW Seven-pass transmembrane receptor; autoimmune disease;
 KM white blood cell dysfunction.
 XX
 OS Homo sapiens.
 XX
 PN WO933876-A1.
 PD 08-JUL-1999.
 XX
 PF 24-DEC-1998; 98MO-JP005886.
 XX
 PR 24-DEC-1997; 97JP-00354537.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 PI Ohno T, Koshio T, Ishimaru H;
 XX
 DR MPI: 1999-493806/41.
 DR N-PSDB; AAY86674.
 XX
 PT New seven-pass transmembrane receptor protein useful for treating,
 XX preventing or diagnosing autoimmune diseases.
 XX
 PS Claim 1; Page 101-103; 118pp; Japanese.
 XX
 CC The present sequence represents a seven-pass transmembrane receptor
 CC protein. The protein and its DNA can be used to screen substances for the
 CC diagnosis, prevention and treatment of autoimmune diseases, particularly
 CC those due to white blood cell dysfunction
 XX
 SQ Sequence 350 AA;

QY 1 MALEONQSTDYEEENNGTYDYSQYELICKEVDREFAKFLPVFLTVFVIGLAGNS 60
 DB 1 MALEONQSTDYEEENNGTYDYSQYELICKEVDREFAKFLPVFLTVFVIGLAGNS 60
 QY 61 MVAIAIYKQKRTKDVIILMLAVADLLFLTFPMWANAAGWLGKIMKITSALYT 120
 DB 61 MVAIAIYKQKRTKDVIILMLAVADLLFLTFPMWANAAGWLGKIMKITSALYT 120
 QY 121 NFVSGMOFLACISIDRYAVATKVPQSGVGKPCWIIICCVMAAILLSIPOLVFTVND 180
 DB 121 NFVSGMOFLACISIDRYAVATKVPQSGVGKPCWIIICCVMAAILLSIPOLVFTVND 180
 QY 181 NARCTIFPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNIXSRPLK 240
 DB 181 NARCTIFPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNIXSRPLK 240
 QY 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLTSCNMSKRMIDIAIQVTESIALFHSCLNP 300
 DB 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLTSCNMSKRMIDIAIQVTESIALFHSCLNP 300
 QY 301 ILYVFMGASFKNYVMKVAKKYGSWRQROSVBEPDSEGPTEPTSTFSI 350
 DB 301 ILYVFMGASFKNYVMKVAKKYGSWRQROSVBEPDSEGPTEPTSTFSI 350

RESULT 14
 ID AAB02835
 AC AAB02835 standard; protein; 350 AA.
 XX AAB02835;
 XX
 DT 22-AUG-2000 (first entry)
 DE Human G protein coupled receptor hEP1 protein SEQ ID NO:24.
 XX
 KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
 KM identification; agonist; screening; therapeutic; pharmaceutical; mutant.
 XX
 OS Homo sapiens.
 XX
 PN WO200022131-A2.
 PD 20-APR-2000.
 XX
 PF 13-OCT-1999; 99MO-US024065.
 XX
 PR 13-OCT-1998; 98US-00170496.
 XX
 PR 12-NOV-1998; 98US-0108029P.
 XX
 PR 20-NOV-1998; 98US-0109213P.
 XX
 PR 27-NOV-1998; 98US-0110060P.
 XX
 PR 16-FEB-1999; 99US-0120416P.
 XX
 PR 26-FEB-1999; 99US-0121852P.
 XX
 PR 12-MAR-1999; 99US-0123944P.
 XX
 PR 12-MAR-1999; 99US-0123945P.
 XX
 PR 12-MAR-1999; 99US-0123946P.
 XX
 PR 12-MAR-1999; 99US-0123948P.
 XX
 PR 12-MAR-1999; 99US-0123949P.
 XX
 PR 12-MAR-1999; 99US-0123951P.
 XX
 PR 28-MAY-1999; 99US-0136436P.
 XX
 PR 28-MAY-1999; 99US-0136437P.
 XX
 PR 28-MAY-1999; 99US-0136439P.
 XX
 PR 28-MAY-1999; 99US-0137127P.
 XX
 PR 28-MAY-1999; 99US-0137313P.
 XX
 PR 28-MAY-1999; 99US-0137567P.
 XX
 PR 29-JUN-1999; 99US-0141448P.
 XX
 PR 27-AUG-1999; 99US-0151114P.
 XX
 PR 03-SEP-1999; 99US-0152524P.
 XX
 PR 29-SEP-1999; 99US-0156555P.

PR 29-SEP-1999; 99US-0156633P.
 PR 29-SEP-1999; 99US-0156634P.
 PR 29-SEP-1999; 99US-0156635P.
 PR 01-OCT-1999; 99US-0157280P.
 PR 01-OCT-1999; 99US-0157281P.
 PR 01-OCT-1999; 99US-0157282P.
 PR 01-OCT-1999; 99US-0157283P.
 PR 01-OCT-1999; 99US-0157294P.
 PR 12-OCT-1999; 99US-00416760.
 PR 12-OCT-1999; 99US-00417044.

PA (AREN-) ARENA PHARM INC.

PI Behan DP, Lehmann-Bruhnsma K, Chalmers DT, Chen R, Dang HT;
 PI Gore M, Liaw CW, Lin I, Lowitz K, White C;

DR WPI; 2000-317986/27.
 DR N-PSDB; AAA46029.

PT Non-endogenous, human G protein-coupled receptors for screening receptor,
 PT inverse or partial agonists useful as therapeutic agents.

XX Example 1; Page 99-100; 187pp; English.

XX The present invention describes transmembrane receptors, preferably human
 CC G protein coupled receptors (GPCR), for which the endogenous ligand is
 CC unknown (orphan GPCR receptors). More specifically the present invention
 CC relates to non-endogenous, constitutively activated versions of a human
 CC GPCR. These non-endogenous human GPCRs can be useful for the direct
 CC identification of candidate compounds as receptor agonists, inverse
 CC agonists or partial agonists for use as pharmaceutical agents. AAA46017
 CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the
 CC exemplification of the present invention

XX Sequence 350 AA;

SQ Query Match 99.5%; Score 1810; DB 3; Length 350;
 Best Local Similarity 99.4%; Pred. No. 8.9e-194;

Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 M A L E N O S T D Y Y E N E N N G T Y D Y S Q Y E L I C K E D V R E F A V P L P V L T I V I V I G L A G N S 60
 DB 1 M A L E N O S T D Y Y E N E N N G T Y D Y S Q Y E L I C K E D V R E F A V P L P V L T I V I V I G L A G N S 60
 QY 61 M V A I Y A Y K K O R T D V Y I I N L A V A D L L F T L P F M A V N A H G V L G K I M C K I T S A L Y T 120
 DB 61 M V A I Y A Y K K O R T D V Y I I N L A V A D L L F T L P F M A V N A H G V L G K I M C K I T S A L Y T 120
 QY 121 L N F V S G M O F L A C I S I D R Y V A V T K V P S G V G K P C W I I C F C W M A A I L I S I P Q L V F Y T V N D 180
 DB 121 L N F V S G M O F L A C I S I D R Y V A V T K V P S G V G K P C W I I C F C W M A A I L I S I P Q L V F Y T V N D 180
 QY 181 N A R C P I P R Y L G T S M K A L I O M L E I C I G F V V P F L I M G V C Y T I T A T K M K N I K S R P L K 240
 DB 181 N A R C P I P R Y L G T S M K A L I O M L E I C I G F V V P F L I M G V C Y T I T A T K M K N I K S R P L K 240
 QY 241 V L L V I V I F I V T O L P N I V K F C R A I D I I Y S L I T S C N S K R M D I A I Q V T E S I A L H S C I N P 300
 DB 241 V L L V I V I F I V T O L P N I V K F C R A I D I I Y S L I T S C N S K R M D I A I Q V T E S I A L H S C I N P 300
 QY 301 I L Y V M G S F K N Y V M K V A K K Y G S W R O R O S V E E F P D S E G T E P T S T S I 350
 DB 301 I L Y V M G S F K N Y V M K V A K K Y G S W R O R O S V E E F P D S E G T E P T S T S I 350

RESULT 15

AAV71301 standard; protein; 350 AA.

AC AAV71301;

DT 02-NOV-2000 (first entry)

XX

DE Human orphan G protein-coupled receptor hppr1.
 XX Human; orphan G protein-coupled receptor; GPCR; hppr1; drug screening;
 KM transmembrane receptor; expressed sequence tag; EST; signal cascade.
 XX Homo sapiens.

XX WO200031258-A2.

XX 02-JUN-2000.

PF 13-OCT-1999; 99WO-US023687.

PR 20-NOV-1998; 98US-0109213P.

PR 16-FEB-1999; 99US-0120416P.

PR 26-FEB-1999; 99US-0121852P.

PR 12-MAR-1999; 99US-0123946P.

PR 12-MAR-1999; 99US-0123949P.

PR 28-MAY-1999; 99US-0136436P.

PR 28-MAY-1999; 99US-0136437P.

PR 28-MAY-1999; 99US-0136439P.

PR 28-MAY-1999; 99US-0136567P.

PR 28-MAY-1999; 99US-0137127P.

PR 28-MAY-1999; 99US-0137131P.

PR 29-JUN-1999; 99US-0141448P.

PR 29-SEP-1999; 99US-0156555P.

PR 29-SEP-1999; 99US-0156633P.

PR 29-SEP-1999; 99US-0156634P.

PR 29-SEP-1999; 99US-0156635P.

PR 01-OCT-1999; 99US-0157280P.

PR 01-OCT-1999; 99US-0157281P.

PR 01-OCT-1999; 99US-0157282P.

PR 01-OCT-1999; 99US-0157293P.

PR 01-OCT-1999; 99US-0157294P.

PR 12-OCT-1999; 99US-00416760.

PR 12-OCT-1999; 99US-00417044.

XX (AREN-) ARENA PHARM INC.

PI Chen R, Dang HT, Liaw CW, Lin I;

DR WPI; 2000-400668/34.

DR N-PSDB; AAD01128.

XX Novel human orphan G protein-coupled receptors and the encoding cDNAs for
 XX use in the identification of G protein-coupled receptor agonists.

QY 1 M A L E N O S T D Y Y E N E N N G T Y D Y S Q Y E L I C K E D V R E F A V P L P V L T I V I V I G L A G N S 60

XX

Db	1	MALEQONSTDYIYEENENGTVDYSQELICIKEDVBEAKVFLPVFLTIAFYIGLAGNS	60
QY	61	MVAIYAYVKKORTKDVTYILNLAVADLLFLTLPEMAVAVHGWVLGKIMCKITSALYT	120
Db	61	MVAIYAYVKKORTKDVTYILNLAVADLLFLTLPEMAVAVHGWVLGKIMCKITSALYT	120
QY	121	LNFSGMQPLACTSIDRYAVTVKVPQSQSVGKPCWIIICFCVMAAILLSIPOLVFTVND	180
Db	121	LNFSGMQPLACTSIDRYAVTVKVPQSQSVGKPCWIIICFCVMAAILLSIPOLVFTVND	180
QY	181	NARCIPIFPRIYLGTSKMLIOMLEICIGFVVPFLIMGVCYFIFARTIMKMPNIIKISRPLX	240
Db	181	NARCIPIFPRIYLGTSKMLIOMLEICIGFVVPFLIMGVCYFIFARTIMKMPNIIKISRPLX	240
QY	241	VLLTVVIVFIVTQLPYNIYVFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSCLNP	300
Db	241	VLLTVVIVFIVTQLPYNIYVFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSCLNP	300
QY	301	ILYVFMGASFKNYVMKVAKKYGSMSROROSVEEFPDSEGPTEPTSTPSI	350
Db	301	ILYVFMGASFKNYVMKVAKKYGSMSROROSVEEFPDSEGPTEPTSTPSI	350

Search completed: April 13, 2004, 13:17:34
Job time : 62 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: April 13, 2004, 13:15:20 ; Search time 23 Seconds

(without alignments)
785.613 Million cell updates/sec

Title: US-09-721-341-2

Perfect score: 1819
Sequence: 1 MALEONOSTDYEEENENG.....VEEPFDSGPTSTPTSTPSI 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	2	US-08-966-316-16
2	1808	99.4	350	4	US-09-556-002-2
3	1620	89.1	350	2	US-08-966-316-18
4	659	36.2	358	1	US-08-153-848-19
5	659	36.2	358	3	US-09-299-843A-19
6	659	36.2	358	4	US-09-088-337B-19
7	659	36.2	358	5	PCT-US93-11153-19
8	659	36.2	378	1	US-08-153-848-15
9	659	36.2	378	3	US-09-299-843A-15
10	659	36.2	378	3	US-09-251-545-1
11	659	36.2	378	4	US-09-088-337B-15
12	659	36.2	378	4	US-09-170-496D-74
13	659	36.2	410	5	PCT-US93-11153-15
14	659	36.2	410	1	US-08-153-848-7
15	659	36.2	410	3	US-09-299-843A-7
16	659	36.2	410	4	US-09-088-337B-7
17	659	36.2	410	5	PCT-US93-11153-7
18	655	36.0	378	4	US-09-170-496D-204
19	650	35.7	378	3	US-09-299-843A-66
20	650	35.7	378	4	US-09-088-337B-66
21	643	35.3	378	1	US-08-383-750-2
22	643	35.3	378	1	US-08-383-751A-2
23	643	35.3	378	3	US-08-352-678-2
24	643	35.3	378	3	US-09-045-583-49
25	643	35.3	378	4	US-09-534-185-49
26	643	35.3	378	4	US-09-536-954-2
27	643	35.3	378	5	PCT-US93-09636-2

28	637	35.0	357	4	US-09-266-464-2	Sequence 2, Appl1
29	637	35.0	357	4	US-09-170-496D-24	Sequence 24, Appl1
30	635.5	34.9	359	1	US-08-153-848-24	Sequence 24, Appl1
31	635.5	34.9	359	3	US-09-299-843A-24	Sequence 24, Appl1
32	635.5	34.9	359	4	US-09-088-337B-24	Sequence 24, Appl1
33	635.5	34.9	359	5	PCT-US93-11153-24	Sequence 24, Appl1
34	631	34.7	357	4	US-09-170-496D-176	Sequence 176, App
35	606.5	33.3	351	2	US-08-902-637-2	Sequence 2, Appl1
36	606.5	33.3	351	3	US-09-178-637-2	Sequence 2, Appl1
37	583	32.1	374	3	US-09-045-583-48	Sequence 48, Appl1
38	583	32.1	374	4	US-09-534-185-48	Sequence 48, Appl1
39	581	31.9	342	3	US-09-116-498-4	Sequence 4, Appl1
40	569	31.3	342	3	US-09-116-498-6	Sequence 6, Appl1
41	560	30.8	342	2	US-08-742-011-2	Sequence 2, Appl1
42	560	30.8	342	3	US-09-275-384B-5	Sequence 5, Appl1
43	560	30.8	342	3	US-09-116-498-2	Sequence 2, Appl1
44	560	30.8	342	4	US-09-449-437A-2	Sequence 2, Appl1
45	560	30.8	342	4	US-09-517-605-9	Sequence 9, Appl1

ALIGNMENTS

RESULT 1
US-08-966-316-16
Sequence 16, Application US/08966316
Patent No. 5932445
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Au-Young, Janice
APPLICANT: Reddy, Roopa
APPLICANT: Murthy, Lynn E.
APPLICANT: Mathur, Preete
TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0424 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: UTRSN0T11
CLONE: 2547002
US-08-966-316-16

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Query Match      100.0%; Score 1819; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.2e-148;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENENNGTYDSQYELICKEDEVEPAKFLPFLITIVFVIGLAGNS 60
DB 1 MALEONOSTDYEEENENNGTYDSQYELICKEDEVEPAKFLPFLITIVFVIGLAGNS 60
QY 61 MVAIAIYAYKKORTKTDVYIILNLAVALDLLFTLPFWAVNAVHGVGLGKIMCKITSALYT 120
DB 61 MVAIAIYAYKKORTKTDVYIILNLAVALDLLFTLPFWAVNAVHGVGLGKIMCKITSALYT 120
QY 121 INFVSGMOPLACISIDRYAVATKVPSSQGVGKPCWIIICFCVMAAIIILISIPQLVFTVND 180
DB 121 INFVSGMOPLACISIDRYAVATKVPSSQGVGKPCWIIICFCVMAAIIILISIPQLVFTVND 180
QY 181 NARCIPIPRYIGTSMKALIQMLEICIGFVVPFLMGVCYFITTARTLMKMNKISRPLK 240
DB 181 NARCIPIPRYIGTSMKALIQMLEICIGFVVPFLMGVCYFITTARTLMKMNKISRPLK 240
QY 241 VLLTVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNP 300
DB 241 VLLTVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNP 300
QY 301 ILVFMGASFKYVWVKAKKYGSMROROSVEEFPDSEGPTEPSTFSI 350
DB 301 ILVFMGASFKYVWVKAKKYGSMROROSVEEFPDSEGPTEPSTFSI 350

RESULT 2
US-09-556-002-2
; Sequence 2, Application us/09556002
; Patent No. 6620615
; GENERAL INFORMATION:
; APPLICANT: Gould-Rouberg, Bonnie
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR AND METHOD OF USING SAME
; FILE REFERENCE: 15966-550
; CURRENT APPLICATION NUMBER: US/09/556,002
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: USSN 60/130,817
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-556-002-2

Query Match      99.4%; Score 1808; DB 4; Length 350;
Best Local Similarity 99.4%; Pred. No. 1.1e-147;
Matches 348; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MALEONOSTDYEEENENNGTYDSQYELICKEDEVEPAKFLPFLITIVFVIGLAGNS 60
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DB 61 MVAIAIYAYKKORTKTDVYIILNLAVALDLLFTLPFWAVNAVHGVGLGKIMCKITSALYT 120
QY 121 INFVSGMOPLACISIDRYAVATKVPSSQGVGKPCWIIICFCVMAAIIILISIPQLVFTVND 180
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DB 181 NARCIPIPRYIGTSMKALIQMLEICIGFVVPFLMGVCYFITTARTLMKMNKISRPLK 240
QY 241 VLLTVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNP 300
DB 241 VLLTVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNP 300

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QY 301 ILVFMGASFKYVWVKAKKYGSMROROSVEEFPDSEGPTEPSTFSI 350
DB 301 ILVFMGASFKYVWVKAKKYGSMROROSVEEFPDSEGPTEPSTFSI 350

RESULT 3
US-08-966-316-18
; Sequence 18, Application us/08966316
; Patent No. 5932445
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: An-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murty, Lynn E.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,316
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: P2-0424 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 399711
US-08-966-316-18

Query Match      89.1%; Score 1620; DB 2; Length 350;
Best Local Similarity 86.0%; Pred. No. 1.5e-131;
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENENNGTYDSQYELICKEDEVEPAKFLPFLITIVFVIGLAGNS 60
DB 1 MALEONOSTDYEEENENNGTYDSQYELICKEDEVEPAKFLPFLITIVFVIGLAGNS 60
QY 61 MVAIAIYAYKKORTKTDVYIILNLAVALDLLFTLPFWAVNAVHGVGLGKIMCKITSALYT 120
DB 61 MVAIAIYAYKKORTKTDVYIILNLAVALDLLFTLPFWAVNAVHGVGLGKIMCKITSALYT 120
QY 121 INFVSGMOPLACISIDRYAVATKVPSSQGVGKPCWIIICFCVMAAIIILISIPQLVFTVND 180
DB 121 INFVSGMOPLACISIDRYAVATKVPSSQGVGKPCWIIICFCVMAAIIILISIPQLVFTVND 180
QY 181 NARCIPIPRYIGTSMKALIQMLEICIGFVVPFLMGVCYFITTARTLMKMNKISRPLK 240
DB 181 NARCIPIPRYIGTSMKALIQMLEICIGFVVPFLMGVCYFITTARTLMKMNKISRPLK 240

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DB 181 KACACVIFPHYHGTSMKASIOLEICIGPIIPFLMAVCYFTTAKTLIMPNIKKSOPK 240
 QY 241 VLTIVIVIVITVQLPNIYKFCRAIDIIYSLTSCNMSKRDIAIQVTEISILFSCNLP 300
 DB 241 VLTIVIVIVITVQLPNIYKFCRAIDIIYSLTSCNMSKRDIAIQVTEISILFSCNLP 300
 QY 301 ILVYFMGASFKNYVMKAKKYGSMRQROSVVEFPDSEGLEPTSTFSI 350
 DB 301 VLYVFMGTSFKNYIMKAKKYGSMRQROSVVEFPDSEGLEPTSTFSI 350

RESULT 4
 US-08-153-848-19
 / Sequence 19, Application US/08153848
 / Patent No. 5759804
 / GENERAL INFORMATION:
 / APPLICANT: Godiska, Ronald
 / APPLICANT: Gray, Patrick W.
 / APPLICANT: Schweikart, Vicki L.
 / TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
 / NUMBER OF SEQUENCES: 64
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 / ADDRESSEE: Bicknell
 / STREET: 6300 Sears Tower, 233 South Wacker Drive
 / CITY: Chicago
 / STATE: Illinois
 / COUNTRY: USA
 / ZIP: 60606
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/153,848
 / FILING DATE:
 / CLASSIFICATION: 514
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/977,452
 / FILING DATE: 17-NOV-1992
 / ATTORNEY/AGENT INFORMATION:
 / NAME: No. 5759804and, Greta E.
 / REGISTRATION NUMBER: 35,302
 / REFERENCE/DOCKET NUMBER: 31794
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (312) 474-6300
 / TELEFAX: (312) 474-0448
 / TELEX: 25-3856
 / INFORMATION FOR SEQ ID NO: 19:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 358 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / US-08-153-848-19

Query Match 36.2%; Score 659; DB 1; Length 358;
 Best Local Similarity 38.7%; Pred. No. 5.1e-49;
 Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

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 DB 1 VCLCQDEVDYDNT--TVDTLFESELCGSKVDYRANKAMFLPMYSIIFVGLNG 57
 QY 61 MVAIAIYAKKORTKTDVYILNLAIVADLLFLPLPFMAVNAVGVWLKIMCKITSAIYT 120
 DB 58 LVVLTIVIVIRKLTMTDYILNLAIVADLLFLPLPMWASAKSNVFGVHFKCLFAIYK 117
 QY 121 LNFVSGNOLACISIRIYAVTKVPS----QSGVKGKPCWICFCWMAAILISIQLYVF 176
 DB 118 MSFSGMLLLLCISIDRYAIVAVSAHRHRAVLLISXLSGVGIMILATVISIDELIYS 177

QY 177 TVNDNA-----RCIPRPVLTGSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKP 231
 DB 178 DLGRSSSEQAMRGSLINEH---VEAFITIQVAGVIGFVPLAMSPCYLIIIRTLQAR 234
 QY 232 NIKISRPKLVLIVIVIFITVQLPNIYKFCRAIDIIYSLTSCNMSKRDIAIQVTEI 291
 DB 235 NFEENKAIKVIAVAVVIFVQLPYNGVLAQVAVNFNTSSITCELSKOLNIAVDVYSL 294
 QY 292 ALFHSCLNPLIYVFMGASFKNYVMKAKKYG-----SM-----RROQSVVEFPFD 337
 DB 295 ACVACCVNPFYARIVGVKFRNDLFKFLKDLGCLSQEQLRQMSGRHRRASMSVE----- 349
 QY 338 SEGTEPPTSTFS 349
 DB 350 ---AETTTFS 357

RESULT 5
 US-09-299-843A-19
 / Sequence 19, Application US/09299843A
 / Patent No. 6107475
 / GENERAL INFORMATION:
 / APPLICANT: Godiska, Ronald
 / APPLICANT: Gray, Patrick W.
 / APPLICANT: Schweikart, Vicki L.
 / TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
 / NUMBER OF SEQUENCES: 66
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 / ADDRESSEE: Borun
 / STREET: 6300 Sears Tower, 233 South Wacker Drive
 / CITY: Chicago
 / STATE: Illinois
 / COUNTRY: USA
 / ZIP: 60606
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/299,843A
 / FILING DATE:
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 09/088,337
 / FILING DATE: 01-JUN-1998
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 08/153,848
 / FILING DATE: 17-NOV-1993
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/977,452
 / FILING DATE: 17-NOV-1992
 / ATTORNEY/AGENT INFORMATION:
 / NAME: J111 E. Utl
 / REGISTRATION NUMBER: 43,213
 / REFERENCE/DOCKET NUMBER: 27866/32059B
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (312) 474-6300
 / TELEFAX: (312) 474-0448
 / TELEX:
 / INFORMATION FOR SEQ ID NO: 19:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 358 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / US-09-299-843A-19

Query Match 36.2%; Score 659; DB 3; Length 358;
 Best Local Similarity 38.7%; Pred. No. 5.1e-49;
 Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

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QY      1  M A L E O N S T D Y Y E N E M N G T Y D S O Y E L I C I K E D V R E P A K V L P V F L I T V F I G L A G N S 60
Db      1  V C L C O D E V T D D Y I G D N T --- T V D Y T L F E S I C S K D V N F K A M F L P I M Y S I I C F V G L I G N G 57
QY      61  M V A I A Y A Y K K O R K T D V Y I L N I A V A D L L L F T L P F M A V A N A V H G W I G K I M C K I T S A L Y T 120
Db      58  L V L Y T I Y F R K L T M D T Y I L N I A V A D I L F L L T L P F M A S A A S W V G V H F C K L I A I Y K 117
QY      121  L N F V S G M O F L A C I S I D R Y V A V T K V P S --- Q S G V K P C W I C F C W M A A L I L S I P O L V F Y 176
Db      118  M S F S G M L L I C I S I D R Y V A I V Q A V S A H R H A R V L I S K L S C V G I W I L A T V L S I P E L L Y S 177
QY      177  T V N D N A --- R C I P I F P R Y I G T S M K A L I O M L E I C I G F V V P F L M G C Y F I T A T L M K M P 231
Db      178  D L Q R S S E Q A M R C S L I T E H --- V E A F I T T I O V A Q W I G F L V P L L A M S F C Y L V I I R T L L Q A R 234
QY      232  N I K I S R P L K V L I V V I F I V T O L P N I V K F C R A I D I I Y S L I T S C M S K R M D I A I Q V T E S I 291
Db      235  N F E R N K A I K V I I A V V V F I V F O L P Y N G V V L A Q T A N F N I T S T C E L S K O L N I A Y D V T Y S L 294
QY      292  A L F H S C N P I L Y Y M G A S F K N Y V M K V A K K Y G --- S W --- R R O R O S V E E P F P D 337
Db      295  A C V R C C N P F L Y A I G V K F R N D L F K L F K D G C L S Q E O L R O M S S C R H I R R S M S V E --- 349
QY      338  S E G P T E P T S T F S 349
Db      350  --- A E T T T T F S 357

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RESULT 6

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US-09-088-337B-19
Sequence 19, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids

```

```

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-088-337B-19
Query Match 36.2%; Score 659; DB 4; Length 358;
Best Local Similarity 38.7%; Pred. No. 5,1e-48;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
1 M A L E O N S T D Y Y E N E M N G T Y D S O Y E L I C I K E D V R E P A K V L P V F L I T V F I G L A G N S 60
1 V C L C O D E V T D D Y I G D N T --- T V D Y T L F E S I C S K D V N F K A M F L P I M Y S I I C F V G L I G N G 57
QY      61  M V A I A Y A Y K K O R K T D V Y I L N I A V A D L L L F T L P F M A V A N A V H G W I G K I M C K I T S A L Y T 120
Db      58  L V L Y T I Y F R K L T M D T Y I L N I A V A D I L F L L T L P F M A S A A S W V G V H F C K L I A I Y K 117
QY      121  L N F V S G M O F L A C I S I D R Y V A V T K V P S --- Q S G V K P C W I C F C W M A A L I L S I P O L V F Y 176
Db      118  M S F S G M L L I C I S I D R Y V A I V Q A V S A H R H A R V L I S K L S C V G I W I L A T V L S I P E L L Y S 177
QY      177  T V N D N A --- R C I P I F P R Y I G T S M K A L I O M L E I C I G F V V P F L M G C Y F I T A T L M K M P 231
Db      178  D L Q R S S E Q A M R C S L I T E H --- V E A F I T T I O V A Q W I G F L V P L L A M S F C Y L V I I R T L L Q A R 234
QY      232  N I K I S R P L K V L I V V I F I V T O L P N I V K F C R A I D I I Y S L I T S C M S K R M D I A I Q V T E S I 291
Db      235  N F E R N K A I K V I I A V V V F I V F O L P Y N G V V L A Q T A N F N I T S T C E L S K O L N I A Y D V T Y S L 294
QY      292  A L F H S C N P I L Y Y M G A S F K N Y V M K V A K K Y G --- S W --- R R O R O S V E E P F P D 337
Db      295  A C V R C C N P F L Y A I G V K F R N D L F K L F K D G C L S Q E O L R O M S S C R H I R R S M S V E --- 349
QY      338  S E G P T E P T S T F S 349
Db      350  --- A E T T T T F S 357

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RESULT 7

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PCT-US93-11153-19
Sequence 19, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:

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Tue Apr 13 15:19:22 2004

us-09-721-341-2.rail

Page 5

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1 TELEPHONE: (312) 474-6300
2 TELEFAX: (312) 474-0448
3 TELEX: 25-3865
4
5 INFORMATION FOR SEQ ID NO: 19
6
7 SEQUENCE CHARACTERISTICS:
8     LENGTH: 358 amino acids
9     TYPE: amino acid
10    TOPOLOGY: linear
11
12    MOLECULE TYPE: protein
13
14    PCT-US93-11153-15

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Query Match	36.2%;	Score 659;	DB 5;	Length 358;
Best Local Similarity	38.7%;	Pred. No. 5.1e-49;		
Matches 144; Conservative	66;	Mismatches 124;	Indels 38;	Gaps 7

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QY      1 M A L E Q U O S T D Y Y A E E N N G M G J V D Y S Q Y E L I C K E D V R E F A V F L P V E L T I F V G I A G N S   60
Db      1 V C L C O D E V D D I G D N T --- T V D Y T L F B E L C S K D V R F K A M F L P I M S I I C F V G L G N G   57
QY      61 M V A I Y A Y Y K K O R T K D T Y I I N L A V A D L L E T P E F M A V N A V H G V L G K I M C K I T S A L Y T   120
Db      58 I A V L T I Y F R K R I K T M D T Y L I N L A V A D I L F L T L P F M A Y S A K S A V S E V H C K I I P A I Y K   117
QY      121 L N F V S G M Q L A C I S I D R I Y A V T K V S --- Q S G V K P C W I T C F C V M A A I I L S I P O V F Y   176
Db      118 M S F F S M L L I C I S I D R Y A I V O A S A H R H A R V L L I S K L C V G I M I L A T A L S I P E L L Y S   177
QY      177 T Y V D N A --- R C I P I F R Y L G T S K A L I O M E I G I G V N V F L I N G V Y F T A T L M K M P   233
Db      178 D I O R S S E Q M R C S L I T E H --- V E A F T T I Q A Q W I G L V P L M A S F C Y L V I T F T L Q A R   234
QY      232 N K I S R P L K V L L T V I V I P T O L P Y N I V K F C R A I D I I S L T S C M S K R M D I A I Q V T E S I   291
Db      235 N E R N K A I V I I A V V V F I V P O L P I N G V L A Q T A N F N I T S T C E L S K Q L N I A D V Y S L   296
QY      292 A L F H S L A N D I L Y F N G A S F K N Y V M K V A K K Y G --- S W --- R R O R Q S V E E F P F D   337
Db      295 A C V R C C V N F L A F I G V K F R N D L F K L F K D L G C L S Q E Q L R O M S S C R H I R R S M S V E ---   349
QY      338 S E G P T E P T S F S   349
Db      350 --- A E T T I T F S   357

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RESULT 8
US-08-153-848-15
; Sequence 15, Application US/08153848
Data: US-08153-848-15

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1      FILING DATE: 17-NOV-1992
2      *AUTHOR/AGENT INFORMATION:
3      NAME: No. 5759804and, Great
4      REGISTRATION NUMBER: 35,333
5      REFERENCE/DOCKET NUMBER: 1
6      TELECOMMUNICATION INFORMATION
7      TELEPHONE: (312) 474-6300
8      TELEFAX: (312) 474-0448
9      TELEX: 25-3856
10     INFORMATION FOR SEQ ID NO: 15
11     SEQUENCE CHARACTERISTICS:
12     LENGTH: 378 amino acids
13     TYPE: amino acid
14     TOPOLOGY: linear
15     MOLECULE TYPE: protein
16
17     US-08-153-848-15

```

Query Match	36.2%;	Score 659;	DB 1;	Length 378;
Best Local Similarity	38.7%;	Pred. No. 5.4e-49;		
Matches 144;	Conservative 66;	Mismatches 124;	Indels 38;	Gaps 7;

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QY      : MLEQOSQSDIYYEENEMNGTADYXQYQLICIKEDVREPAKVFLEPVLLIVAVYGLAGNS 60
Db      21 VCLCQDEVTDEIDYIGNT---IVDYTLPEFSLCKSDVNRFRAMFLPIPIYSLICEVGLGNG 77

QY      61 MYVAIYAYYKQRTQTDVYIINLAVADLLLETLPEMAVNAVHGMVLGKIMCKITSAIYLT 120
Db      78 LVVLITVYFKRKJMTQDTYLLNLINLAVADILFLLTLPEMAVNSAASKSVNGVHFKCKILFAYIK 137

QY      121 LMFVSGMOJLACISIDRYVAATKTPS---QSGXGKWCWIIICFCVMAAILLISIPQVIFY 176
Db      138 MSFESGMLLLICISIDRYVAIVQAVSAHRHARFARLLISKSCVGIWIAVLVSLPIELIYS 197

QY      177 IVNDNA-----RCIPFPRVLTGSMKALIQMLQMLCIGFVVPFLMIGVCYFTLARTLLKMP 231
Db      198 DLRSSSEQANRCSLITEH---VEAFITIQVQVAVIGELVPLMAGSCYVITRITLLQAR 254

QY      232 NIKISPELVLLTVVIVEIVTQLPYNIVKFCRAIDILYSITSCSNMKSMDIAIOVTESTI 291
Db      255 NEERNAKAIKVIIAAVVVVEIVFQLPNGVLAQTVAANNTISSTGELSKQILINAVDYLSL 314

QY      292 ALPHSCINPILIVFNGASFXYVMKVAKYG-----SW-----RQRQSYEEPPFD 357
Db      315 ACVRCQVNPFLVAFVGVKFRNDLFKLFDGLGCSQEOQLROMSSGRHIRRSSMSVE----- 369

QY      338 SSGPTPEPTSTS 349
Db      370 ----AETITTS 377

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RESULT 9
US-09-299-843A-15
Sequence 15. Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptor
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0., Version #1.25


```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/259,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: JILL E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-259-843A-15

Query Match      36.2%; Score 659; DB 3; Length 378;
Best Local Similarity 38.7%; Pred. No. 5,4e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 M A L E Q N S T D Y Y E E N M N G T Y D S Q Y E L I C K E D Y R E F A K V L P V F L T I V F V I G L A G N S 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 21 V C L C D E V T D D Y I G D N T - - - T V D Y T L F E S L C S K D V R N F K A M F L P I M S I I C F V G L L G N G 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 M V A I A Y A Y K K O R T K T D V T I L N A V A D L L F T L P F M A V N A V H G W L G K I M C K I T S A L Y T 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 78 L V A L T Y I F E R K L T M D T Y L N L A V A D I L F L T L P F M A Y S A K S W F G V H F C K L I F A I Y K 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 121 I N F V S G M Q F L A C I S I D R Y A V A V T K V P S - - - Q S G V K P C W I I C F C V M A A I L I S P O L V E Y 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 138 M S F F S G M L L I C I S I D R Y A I V A Q A V S A H R H R A R V L I S K L S C V G I W I A T V L S I P E L L Y S 197
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QY 177 T V N D N A - - - - R C I P F P R Y L G T S M K A L I O M L E I C I G F V P P L I M G V C Y F T A R T L M K P 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 198 D L O R S S E Q A M R C S L I T E H - - - V E A F I T I V A Q W I G F I V P L A M S F C Y L V I R T L L Q A R 254
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 232 N I K I S R P L K V L T V I V F I V T O L P Y N I V K F C R A I D I I Y S L I T S C M S K M D I A I Q Y T E S I 291
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 255 N F E R N A I K I A I V A V V F I V F O L P Y N G V L A Q T V A N F N I T S C E L S K O L N I A D V T Y S L 314
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 292 A L F H S C L N P L I V F M G A S F K N Y M K V A K K Y G - - - - S W - - - - - R R O S V E E P F P D 337
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DB 315 A C V R C C V N P F L A F I G V K F R N D L F K L F K O L G C L S Q E Q L R O W S C H R I R S S M S V E - - - - 369
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QY 338 S E G P T E P T S F S 349
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DB 370 - - - - A E T T T F S 377
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-09-251-545-1
Sequence 1, Application US/09251545
Patent No. 6153441
GENERAL INFORMATION:
APPLICANT: Edward R. Appelbaum
APPLICANT: Henry M. Sarau
APPLICANT: John R. White
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN CCR7 RECEPTOR
TITLE OF INVENTION: AND CK-19 LIGAND AND INTERACTION THEREOF

```

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FILE REFERENCE: P50753
CURRENT APPLICATION NUMBER: US/09/251,545
CURRENT FILING DATE: 1999-02-17
EARLIER APPLICATION NUMBER: 60/074,883
EARLIER FILING DATE: 1998-02-17
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 378
TYPE: PRT
ORGANISM: Human
US-09-251-545-1

Query Match      36.2%; Score 659; DB 3; Length 378;
Best Local Similarity 38.7%; Pred. No. 5,4e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 M A L E Q N S T D Y Y E E N M N G T Y D S Q Y E L I C K E D Y R E F A K V L P V F L T I V F V I G L A G N S 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 21 V C L C D E V T D D Y I G D N T - - - T V D Y T L F E S L C S K D V R N F K A M F L P I M S I I C F V G L L G N G 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 M V A I A Y A Y K K O R T K T D V T I L N A V A D L L F T L P F M A V N A V H G W L G K I M C K I T S A L Y T 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 78 L V A L T Y I F E R K L T M D T Y L N L A V A D I L F L T L P F M A Y S A K S W F G V H F C K L I F A I Y K 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 121 I N F V S G M Q F L A C I S I D R Y A V A V T K V P S - - - Q S G V K P C W I I C F C V M A A I L I S P O L V E Y 176
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DB 138 M S F F S G M L L I C I S I D R Y A I V A Q A V S A H R H R A R V L I S K L S C V G I W I A T V L S I P E L L Y S 197
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QY 177 T V N D N A - - - - R C I P F P R Y L G T S M K A L I O M L E I C I G F V P P L I M G V C Y F T A R T L M K P 231
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DB 198 D L O R S S E Q A M R C S L I T E H - - - V E A F I T I V A Q W I G F I V P L A M S F C Y L V I R T L L Q A R 254
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QY 232 N I K I S R P L K V L T V I V F I V T O L P Y N I V K F C R A I D I I Y S L I T S C M S K M D I A I Q Y T E S I 291
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 255 N F E R N A I K I A I V A V V F I V F O L P Y N G V L A Q T V A N F N I T S C E L S K O L N I A D V T Y S L 314
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QY 292 A L F H S C L N P L I V F M G A S F K N Y M K V A K K Y G - - - - S W - - - - - R R O S V E E P F P D 337
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DB 315 A C V R C C V N P F L A F I G V K F R N D L F K L F K O L G C L S Q E Q L R O W S C H R I R S S M S V E - - - - 369
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QY 338 S E G P T E P T S F S 349
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DB 370 - - - - A E T T T F S 377
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RESULT 11
US-09-088-337B-15
Sequence 15, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: Schwelkart, Vicki L.
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>

```



```

; INFORMATION FOR SEQ ID NO: 15
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 378 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
PCT-US93-1153-15

```

Query Match 36.2%; Score 659; DB 5; Length 378;
Best Local Similarity 38.7%; Pred. No. 5,4e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7.

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QY      1 MAMEJQSDIDYAAEENEMNGTVDYQYELICIKEDVREFAKVPFLVFLTVFVGLAGNS 60
Db      21 VCLCQDEVDYDDYDGNLT---TVDYTLFESLCSKQDVRFKMWFLPIMWISLTCFVGLLNG 77
QY      61 MVAIAIYAAKKORTKTDYIYINLAVADLLFTLPFMAVNAHGVWLGIKIMCKITSALYV 120
Db      78 LVVLTVIYFPRRLTKTMDYTLNMLAVADILFLTLTPFMAYSAAKMWGVGHFCKLIIFAIVK 137
QY      121 LNVVSGMQLACSIDRYVAATKVS---QGVGKPCMIICFCVMAAAILLSIPOLVEY 176
Db      138 MSFSGMQLLLCLCISIDRYVAIVQAVSAHRRRLYLLISKSCVGIWTLAVLSPILLYS 197
QY      177 TVVNDN-----RCIPFPRYGLFSKMLIOMLEICIGVDPFLIMGVCYFIATRTMKP 231
Db      198 DLRRSSSEQMRCSLTTEH---VEAFITIQAVQWITGVLVELLMSFCYLIIVIRTLIQAR 254
QY      232 NIKISRPILKVLTVIVIVITQLPYNIVKFCRAIDIIYSLITSQMSKRMIDIAQVTEST 291
Db      255 NFRNRNAIKIIVVVVFIIVQLPBYNGVLAQTAVNFITSCTCELKQXLIADVYSL 314
QY      292 ALHHSCLNPLIYFMASFKAYVMKYAKYG-----SN-----RQRQSYEEEPFD 337
Db      315 ACVRCVNPFLYAFIVKFRNDLFXLFXDLGCLSQEQLRQWSSCRHIIRRSSMYE----- 369
QY      338 SEGTEPTSTFS 349
Db      370 ---AETTTFS 377

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RESULT 14
US-08-153-848-7
Sequence 7, Application US/08153848
Patent No. 5758604
GENERAL INFORMATION:
APPLICANT: Godtska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell, 233 South Wacker Drive
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
TRANSMISSION FOR CTO ID NO. 7

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? INFORMATION FOR SEQ ID NO: 7:
?
? SEQUENCE CHARACTERISTICS:
?
?   LENGTH: 410 amino acids
?   TYPE: amino acid
?   TOPOLOGY: linear
?
?   MOLECULE TYPE: protein
?
? US-08-153,848-7

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Query Match	36.2%;	Score 659;	DB 1;	Length 410;
Best Local Similarity	38.7%;	Pred. No. 5.9e-49;		
Matches 144;	Conservative 66;	Mismatches 124;	Indels 38;	Gaps 7

```

QY      1 MLEBONOSRDYVEENENNGTYDYSOVELLICIKEDYAEPAKVELPVELTIVFVIGLAGS 60
Db      53 VCLCDEWTDYIGNT---TVDYTLBESLCSKDDYANFKAMTLPIMYSLICVGLLNG 109
QY      61 MYVAIYAYYKOKRTDYIILNLAVALDLFLPMAVNAVHGWLCKMTCKITSALT 120
Db      110 LVVLFIYFVKRLKTDYTLNLNLAVALDILFLTPFWAASAAKSWFGVHFCLTIPAIYK 169
QY      121 LNFVSGMOPLACISIDRVAATKTPS-----QSGGKRCWILICCVMAAAILISIPOLVEY 176
Db      170 MSFSGMILLICISIDRVAAIVQAVSARHRAARLLISKUSCVGIWLAVALVISIPELTS 229
QY      177 TYNDNA-----RCPIPFPRYLGTSMAKALIQMLBICIGFVVPFLIMGCVFITARTLMKOP 231
Db      230 DLORSSBQARCSLITEH---VEAFITTIQVAKWIVGFLVPLAMSCVIAVIRTLLOAR 286
QY      232 NIKSRPEKVLTLVVIVIVTOLPKNIVKFCRAIDIIYLSITCSNMSKMDALIQVTEST 291
Db      287 NFEENKAIKVIILAVVVFIVFQLPYNGVLAQTVANENITSSICELSKQJINIIYADYTSI 346
QY      292 ALPHSLINPLIYVEMGASFKAYVAKKAYG-----SW-----RRRQGVVEEPFD 337
Db      347 ACYRCQVNFPLAIFGVFRNDLFLKFLPDIGLCSQEQBLRQWMSCRHITRSSMVE----- 401
QY      338 SEGTEPTSTFS 349
Db      402 ---AETTTFS 409

```

RESULT 15
 US-09-299-843A-7
 Sequence 7, Application US/09299843A
 Patent No. 6107475
 GENERAL INFORMATION:
 APPLICANT: Godiska, Ronald
 APPLICANT: Gray, Patrick W.
 APPLICANT: Schweikart, Vicki L.
 TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptores
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSER: Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/299,843A
 FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: JILL E. UHL
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-7

Query Match 36.2%; Score 659; DB 3; Length 410;
Best Local Similarity 38.7%; Pred. No. 5.9e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEONOSTDYVEEENENMGTVDSOYELICKEDYREPAKVELPYELTIVFVIGLAGNS 60
DB 53 VCLCQDEVTDDYIGDNT---TVDYTFESLCSKQDYRNKAWFLPIWMSIICFVGLGNG 109
QY 61 MVAIAIYAYYKORTKTDVYILNLAVADLLFLTPFMAVAVHGVYLGKIMCKITSALT 120
DB 110 LVVLTIVYFRRLKMTDYLNLAVADILFLTLFPWYSAKSWVFGVHCKLIFAIYK 169
QY 121 LNFVSGMPLACISIDRYAVATKVS---QSGVSKPCWIIICPCVMMAALLSTPOLVY 176
DB 170 MSFSSGMLLLCISIDRYAVAIQAVSAHRRARVLLISKSCVGIWILATVLSIPELYS 229
QY 177 TVVDNA-----RCIPFPRYLGSMKALIQMLEICIGFVVPFLMGVCYFARTIMKP 231
DB 230 DLQSSSEQAMRCSLITEH---VEAFITIQVAGMVGFLVPLAMSGCYLVIIRTLQAR 286
QY 232 NIKISRLKYLTVIVVFIYVTLQPNIVKFCRAIDIIYSLITSQNSKRMIDAIQYTESI 291
DB 287 NERNRAIKYIIAVVVVFIYFQLPYGVVLAQTVANFNITSSFCELSKQINIAVDVYSI 346
QY 292 ALFHSCINPLIVFMGASFNQVYMKVAKKYG-----SM-----RRQROSVEEFPD 337
DB 347 ACVRCCTNPFLYFVIGKFRNDLFLKFDIGCLSQEQLRQWSSCRHIRKSMSEV----- 401
QY 338 SEGPTEPTSTFS 349
DB 402 ---AETTTFS 409

Search completed: April 13, 2004, 13:19:12
Job time: 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2004, 13:16:24 ; Search time 46 Seconds

(without alignments)
2000.615 Million cell updates/sec

Title: US-09-721-341-2

Perfect score: 1819
Sequence: 1 MALEQNSTDYEEENMG.....VEEPFDEGPTPTPSI 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09C_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1819	100.0	350	9	US-09-765-994-2
2	1819	100.0	350	9	US-09-766-338A-8
3	1819	100.0	350	10	US-09-968-433-16
4	1819	100.0	350	14	US-10-282-837-8
5	1819	100.0	350	14	US-10-225-567A-607
6	1819	100.0	350	14	US-10-288-222A-10
7	1819	100.0	350	14	US-10-145-586-8
8	1819	100.0	350	14	US-10-239-423-75
9	1819	100.0	350	15	US-10-407-079-84
10	1814	99.7	349	9	US-09-765-994-4
11	1810	99.5	348	12	US-10-403-161-12
12	1810	99.5	350	14	US-10-272-963-22
13	1810	99.5	350	14	US-10-393-807-22
14	1810	99.5	350	15	US-10-417-820A-74
15	1803	99.1	350	10	US-09-910-695-8

16	1620	89.1	350	10	US-09-968-433-79	Sequence 79, Appl
17	1257	69.1	242	14	US-10-073-885-73	Sequence 73, Appl
18	862	47.4	164	12	US-10-276-774-1532	Sequence 1532, Ap
19	761	41.8	175	9	US-09-764-853-584	Sequence 584, App
20	761	41.8	175	10	US-09-989-442-108	Sequence 108, App
21	761	41.8	175	11	US-09-764-886-59	Sequence 59, Appl
22	761	41.8	175	11	US-09-764-875-798	Sequence 798, App
23	761	41.8	175	14	US-10-073-865-91	Sequence 91, Appl
24	761	41.8	175	14	US-10-103-313-382	Sequence 382, Appl
25	761	41.8	175	14	US-10-073-885-100	Sequence 100, App
26	659	36.2	378	14	US-10-251-385-74	Sequence 74, Appl
27	659	36.2	378	14	US-10-225-567A-68	Sequence 68, Appl
28	659	36.2	378	14	US-10-239-423-70	Sequence 70, Appl
29	659	36.2	378	15	US-10-435-696-48	Sequence 48, Appl
30	659	36.2	475	12	US-10-425-114-56811	Sequence 56811, A
31	655	36.0	378	14	US-10-451-385-204	Sequence 204, App
32	643	35.3	369	14	US-10-239-423-72	Sequence 72, Appl
33	643	35.3	378	14	US-10-164-649-49	Sequence 49, Appl
34	637	35.0	357	9	US-09-903-377-2	Sequence 2, Appl1
35	637	35.0	357	9	US-09-952-385-2	Sequence 2, Appl1
36	637	35.0	357	13	US-09-966-755-2	Sequence 2, Appl1
37	637	35.0	357	13	US-10-000-759A-2	Sequence 2, Appl1
38	637	35.0	357	14	US-10-251-385-24	Sequence 24, Appl
39	637	35.0	357	14	US-10-825-567A-241	Sequence 241, App
40	637	35.0	357	14	US-10-239-423-73	Sequence 73, Appl
41	637	35.0	369	11	US-09-826-509-481	Sequence 481, App
42	631	34.7	357	14	US-10-251-385-176	Sequence 176, App
43	605	33.3	367	12	US-10-244-089-2	Sequence 2, Appl1
44	605	33.3	367	14	US-10-254-089-2	Sequence 2, Appl1
45	583	32.1	369	14	US-10-239-423-69	Sequence 69, Appl

ALIGNMENTS

RESULT 1
US-09-765-994-2
; Sequence 2, Application US/09765994
; Parent No. US20010016336A1
GENERAL INFORMATION:
; APPLICANT: ELIUS, CATHERINE
; TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: GH-70225-C1
; CURRENT APPLICATION NUMBER: US/09/765,994
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/055,895
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: 08/962,922
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 350
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-765-994-2

Query Match 100.0%; Score 1819; DB 9; Length 350;
Best Local Similarity 100.0%; Pred. No. 4; 7e-159;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALEQNSTDYEEENMGSTYDYSQYELICIKEDVREPAKFLPVPLTIVFYIGAGNS 60
DB 1 MALEQNSTDYEEENMGSTYDYSQYELICIKEDVREPAKFLPVPLTIVFYIGAGNS 60
QY 61 MVAIVYVYKQKTKDVTILNLAVALDLLFTLPFAVAVAHGVYLGKIMCITSALT 120
DB 61 MVAIVYVYKQKTKDVTILNLAVALDLLFTLPFAVAVAHGVYLGKIMCITSALT 120
QY 121 LNFVSGNQFLACISIDRYAVTVFSGSGYKPCWIIICPCVMAAILLSIPQLVFYTVD 180
DB 121 LNFVSGNQFLACISIDRYAVTVFSGSGYKPCWIIICPCVMAAILLSIPQLVFYTVD 180
QY 121 LNFVSGNQFLACISIDRYAVTVFSGSGYKPCWIIICPCVMAAILLSIPQLVFYTVD 180
DB 121 LNFVSGNQFLACISIDRYAVTVFSGSGYKPCWIIICPCVMAAILLSIPQLVFYTVD 180

QY 181 NARCIPIFRYLGTSKALIQMLEICIGFVPEFLMGVCYFRTATLMKMPNKRISPLK 240
 DB 181 NARCIPIFRYLGTSKALIQMLEICIGFVPEFLMGVCYFRTATLMKMPNKRISPLK 240
 QY 241 VLLTVVIVIVTQLPNIVKFCRAIDIIYSLITSCNMRKDIAIQVESIALFHSCLNP 300
 DB 241 VLLTVVIVIVTQLPNIVKFCRAIDIIYSLITSCNMRKDIAIQVESIALFHSCLNP 300
 QY 301 ILYVFMGASFKNYVMKAKKYSWROROSVEEFPDSEGPTEPTSTSI 350
 DB 301 ILYVFMGASFKNYVMKAKKYSWROROSVEEFPDSEGPTEPTSTSI 350

RESULT 2

US-09-796-338A-8
 ; Sequence 8, Application US/09796338A
 ; Patent No. US2002006:522A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
 ; TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
 ; FILE REFERENCE: 10448-020001
 ; CURRENT APPLICATION NUMBER: US/09/796,338A
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: US 60/186,059
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 350
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-796-338A-8

Query Match 100.0%; Score 1819; DB 9; Length 350;
 Best Local Similarity 100.0%; Pred. No. 4.7e-158;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENMGTYDSQYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 60
 DB 1 MALEQNSTDYEEENMGTYDSQYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 60
 QY 61 MVAIAYAYKKORTKTDVYILNLAVADLLFLTPFWANAVHGWVLGKIMCKITSALYT 120
 DB 61 MVAIAYAYKKORTKTDVYILNLAVADLLFLTPFWANAVHGWVLGKIMCKITSALYT 120
 QY 121 LNFVSGMQLACISIDRYAVATKVPSSQSGVKPCWIIICFCVMAAILLSIPQLVFTYND 180
 DB 121 LNFVSGMQLACISIDRYAVATKVPSSQSGVKPCWIIICFCVMAAILLSIPQLVFTYND 180
 QY 181 NARCIPIFRYLGTSKALIQMLEICIGFVPEFLMGVCYFRTATLMKMPNKRISPLK 240
 DB 181 NARCIPIFRYLGTSKALIQMLEICIGFVPEFLMGVCYFRTATLMKMPNKRISPLK 240
 QY 241 VLLTVVIVIVTQLPNIVKFCRAIDIIYSLITSCNMRKDIAIQVESIALFHSCLNP 300
 DB 241 VLLTVVIVIVTQLPNIVKFCRAIDIIYSLITSCNMRKDIAIQVESIALFHSCLNP 300
 QY 301 ILYVFMGASFKNYVMKAKKYSWROROSVEEFPDSEGPTEPTSTSI 350
 DB 301 ILYVFMGASFKNYVMKAKKYSWROROSVEEFPDSEGPTEPTSTSI 350

RESULT 3

US-09-968-433-16
 ; Sequence 16, Application US/09968433
 ; Publication No. US20030073162A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Au-Yang, Janice
 ; APPLICANT: Reddy, Koopa
 ; APPLICANT: Murty, Lynn E.

APPLICANT: Mathur, Preeti
 ; TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING PROTEINS
 ; FILE REFERENCE: PC-0051 CIP
 ; CURRENT APPLICATION NUMBER: US/09/968,433
 ; CURRENT FILING DATE: 2001-10-01
 ; NUMBER OF SEQ ID NOS: 79
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 16
 ; LENGTH: 350
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. US20030073162A1 2547002CD1
 US-09-968-433-16

Query Match 100.0%; Score 1819; DB 10; Length 350;
 Best Local Similarity 100.0%; Pred. No. 4.7e-158;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENMGTYDSQYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 60
 DB 1 MALEQNSTDYEEENMGTYDSQYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 60
 QY 61 MVAIAYAYKKORTKTDVYILNLAVADLLFLTPFWANAVHGWVLGKIMCKITSALYT 120
 DB 61 MVAIAYAYKKORTKTDVYILNLAVADLLFLTPFWANAVHGWVLGKIMCKITSALYT 120
 QY 121 LNFVSGMQLACISIDRYAVATKVPSSQSGVKPCWIIICFCVMAAILLSIPQLVFTYND 180
 DB 121 LNFVSGMQLACISIDRYAVATKVPSSQSGVKPCWIIICFCVMAAILLSIPQLVFTYND 180
 QY 181 NARCIPIFRYLGTSKALIQMLEICIGFVPEFLMGVCYFRTATLMKMPNKRISPLK 240
 DB 181 NARCIPIFRYLGTSKALIQMLEICIGFVPEFLMGVCYFRTATLMKMPNKRISPLK 240
 QY 241 VLLTVVIVIVTQLPNIVKFCRAIDIIYSLITSCNMRKDIAIQVESIALFHSCLNP 300
 DB 241 VLLTVVIVIVTQLPNIVKFCRAIDIIYSLITSCNMRKDIAIQVESIALFHSCLNP 300
 QY 301 ILYVFMGASFKNYVMKAKKYSWROROSVEEFPDSEGPTEPTSTSI 350
 DB 301 ILYVFMGASFKNYVMKAKKYSWROROSVEEFPDSEGPTEPTSTSI 350

RESULT 4

US-10-282-837-8
 ; Sequence 8, Application US/10282837
 ; Publication No. US20030082738A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
 ; TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
 ; FILE REFERENCE: 10448-020001
 ; CURRENT APPLICATION NUMBER: US/10/282,837
 ; PRIOR FILING DATE: 2002-10-29
 ; PRIOR APPLICATION NUMBER: US/09/796,338
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: US 60/186,059
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 350
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-282-837-8

Query Match 100.0%; Score 1819; DB 14; Length 350;
 Best Local Similarity 100.0%; Pred. No. 4.7e-158;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENMGTYDSQYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 60

Db 1 MALEONQSTDIYEEENENNGTYDYSQYELICIKEDVREFAKVLPVFLTIVFVIGLAGNS 60

QY 61 MVAIAIYAYKKORTKTDVYILNLAVADLLFLTPFWAVNAHGVWGKIMCKITSALYT 120

Db 61 MVAIAIYAYKKORTKTDVYILNLAVADLLFLTPFWAVNAHGVWGKIMCKITSALYT 120

QY 121 LNFVSGMQFLACISIDRYAVATKVPQSOGVSKPCWIIICFCVMAAILLISIPOLVFTYND 180

Db 121 LNFVSGMQFLACISIDRYAVATKVPQSOGVSKPCWIIICFCVMAAILLISIPOLVFTYND 180

QY 181 NARCIPIFRYIGTSMKALIQMLEICIGFVVPFLMGVCYFITTARTLMKMPNIKISRLK 240

Db 181 NARCIPIFRYIGTSMKALIQMLEICIGFVVPFLMGVCYFITTARTLMKMPNIKISRLK 240

QY 241 VLLTVIVIVITQLPYNIYKFCRAIDIIYSLITSCNMSKMDIAIQTESIALFHSCLNP 300

Db 241 VLLTVIVIVITQLPYNIYKFCRAIDIIYSLITSCNMSKMDIAIQTESIALFHSCLNP 300

QY 301 ILVYFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEGPTEPTSTFSI 350

Db 301 ILVYFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEGPTEPTSTFSI 350

RESULT 5

US-10-225-567A-607

Sequence 607, Application US/10225567A

Publication No. US20030113798A1

GENERAL INFORMATION:

APPLICANT: Lifespan Biosciences

APPLICANT: Brown, Joseph P.

APPLICANT: Burner, Glenna C.

APPLICANT: Roush, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 1920-4-4

CURRENT APPLICATION NUMBER: US/10/225,567A

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/257,144

NUMBER OF SEQ ID NOS: 2292

SOFTWARE: PatentIn version 3.1

SEQ ID NO 607

LENGTH: 350

TYPE: PRT

ORGANISM: Homo sapiens

US-10-225-567A-607

Query Match 100.0%; Score 1819; DB 14; Length 350;

Best Local Similarity 100.0%; Pred. No. 4.7e-158; Indels 0; Gaps 0;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONQSTDIYEEENENNGTYDYSQYELICIKEDVREFAKVLPVFLTIVFVIGLAGNS 60

Db 1 MALEONQSTDIYEEENENNGTYDYSQYELICIKEDVREFAKVLPVFLTIVFVIGLAGNS 60

QY 61 MVAIAIYAYKKORTKTDVYILNLAVADLLFLTPFWAVNAHGVWGKIMCKITSALYT 120

Db 61 MVAIAIYAYKKORTKTDVYILNLAVADLLFLTPFWAVNAHGVWGKIMCKITSALYT 120

QY 121 LNFVSGMQFLACISIDRYAVATKVPQSOGVSKPCWIIICFCVMAAILLISIPOLVFTYND 180

Db 121 LNFVSGMQFLACISIDRYAVATKVPQSOGVSKPCWIIICFCVMAAILLISIPOLVFTYND 180

QY 181 NARCIPIFRYIGTSMKALIQMLEICIGFVVPFLMGVCYFITTARTLMKMPNIKISRLK 240

Db 181 NARCIPIFRYIGTSMKALIQMLEICIGFVVPFLMGVCYFITTARTLMKMPNIKISRLK 240

QY 241 VLLTVIVIVITQLPYNIYKFCRAIDIIYSLITSCNMSKMDIAIQTESIALFHSCLNP 300

Db 241 VLLTVIVIVITQLPYNIYKFCRAIDIIYSLITSCNMSKMDIAIQTESIALFHSCLNP 300

QY 301 ILVYFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEGPTEPTSTFSI 350

Db 301 ILVYFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEGPTEPTSTFSI 350

Db 301 ILVYFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEGPTEPTSTFSI 350

RESULT 6

US-10-288-222A-10

Sequence 10, Application US/10288222A

Publication No. US20030119742A1

GENERAL INFORMATION:

APPLICANT: Logan, Thomas Joseph

APPLICANT: Galvin, Katherine

APPLICANT: Chun, Mayoung

TITLE OF INVENTION: Methods and Compositions to treat

TITLE OF INVENTION: Cardiovascular Disease Using 139, 258, 1261, 1486, 2398, 2414,

FILE REFERENCE: MP12001-286P(RM)

CURRENT APPLICATION NUMBER: US/10/288,222A

CURRENT FILING DATE: 2002-11-05

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10

LENGTH: 350

TYPE: PRT

ORGANISM: Homo Sapien

US-10-288-222A-10

Query Match 100.0%; Score 1819; DB 14; Length 350;

Best Local Similarity 100.0%; Pred. No. 4.7e-158; Indels 0; Gaps 0;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONQSTDIYEEENENNGTYDYSQYELICIKEDVREFAKVLPVFLTIVFVIGLAGNS 60

Db 1 MALEONQSTDIYEEENENNGTYDYSQYELICIKEDVREFAKVLPVFLTIVFVIGLAGNS 60

QY 61 MVAIAIYAYKKORTKTDVYILNLAVADLLFLTPFWAVNAHGVWGKIMCKITSALYT 120

Db 61 MVAIAIYAYKKORTKTDVYILNLAVADLLFLTPFWAVNAHGVWGKIMCKITSALYT 120

QY 121 LNFVSGMQFLACISIDRYAVATKVPQSOGVSKPCWIIICFCVMAAILLISIPOLVFTYND 180

Db 121 LNFVSGMQFLACISIDRYAVATKVPQSOGVSKPCWIIICFCVMAAILLISIPOLVFTYND 180

QY 181 NARCIPIFRYIGTSMKALIQMLEICIGFVVPFLMGVCYFITTARTLMKMPNIKISRLK 240

Db 181 NARCIPIFRYIGTSMKALIQMLEICIGFVVPFLMGVCYFITTARTLMKMPNIKISRLK 240

QY 241 VLLTVIVIVITQLPYNIYKFCRAIDIIYSLITSCNMSKMDIAIQTESIALFHSCLNP 300

Db 241 VLLTVIVIVITQLPYNIYKFCRAIDIIYSLITSCNMSKMDIAIQTESIALFHSCLNP 300

QY 301 ILVYFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEGPTEPTSTFSI 350

Db 301 ILVYFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEGPTEPTSTFSI 350

RESULT 7

US-10-145-586-8

Sequence 8, Application US/10145586

Publication No. US20030138690A1

GENERAL INFORMATION:

APPLICANT: Alexandra Glucksmann, Maria

APPLICANT: Silos-Santlago, Immaculada

APPLICANT: M. Galvin, Katherine

APPLICANT: Welch, Nadine

APPLICANT: Curtis, Rory A. J.

APPLICANT: Bandaru, Rajasekhar

APPLICANT: Kapeller-Liebermann, Rosana

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS.

TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH

FILE REFERENCE: 10448-188001

CURRENT APPLICATION NUMBER: US/10/145,586

CURRENT FILING DATE: 2002-05-14

Prior Application removed - See file Wrapper or Palm

NUMBER OF SEQ ID NOS: 95
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 8
LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
US-10-145-586-8

Query Match 100.0%; Score 1819; DB 14; Length 350;
Best Local Similarity 100.0%; Pred. No. 4,7e-158;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEQNSTDYEEENMGTYDYSQYELICKEDEVEFAKFLPVFLTIVFVIGLAGNS 60
DB 1 MLEQNSTDYEEENMGTYDYSQYELICKEDEVEFAKFLPVFLTIVFVIGLAGNS 60
QY 61 MVAIAYAYKKORTKIDYIILNLAVADLLFLTPFWANAVHGVWLGKIMCKITSALT 120
DB 61 MVAIAYAYKKORTKIDYIILNLAVADLLFLTPFWANAVHGVWLGKIMCKITSALT 120
QY 121 LNFVSGMOFLACISIDRYAVATKVPSSQSGVGPWCWICFCVMAAILLSIPOLVFYTVND 180
DB 121 LNFVSGMOFLACISIDRYAVATKVPSSQSGVGPWCWICFCVMAAILLSIPOLVFYTVND 180
QY 181 NARCIPIPRVIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKMPNIXISRLK 240
DB 181 NARCIPIPRVIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKMPNIXISRLK 240
QY 241 VLLTVIVIVITQLPYNIVKFCRAIDIIYSLITSCMSKRMIDAIQVTSIALFHSCLNP 300
DB 241 VLLTVIVIVITQLPYNIVKFCRAIDIIYSLITSCMSKRMIDAIQVTSIALFHSCLNP 300
QY 301 ILVFMGASFKNYVMKAKKYSWRRORSVEEFPDSGTEPTSTPSI 350
DB 301 ILVFMGASFKNYVMKAKKYSWRRORSVEEFPDSGTEPTSTPSI 350

RESULT 8

US-10-239-423-75
Sequence 75, Application US/10239423
Publication No. US20030186889A1
GENERAL INFORMATION:
APPLICANT: FORSMANN, Wolf-Georg; FORSMANN, Ulf; ABERMANN, Knut;
APPLICANT: HEITLAND, Aleksandra; SODSBERG, Nikola
TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
FILE REFERENCE: 022217us
CURRENT APPLICATION NUMBER: US/10/239,423
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: DE10016013.1
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 75
LENGTH: 350
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-75

Query Match 100.0%; Score 1819; DB 14; Length 350;
Best Local Similarity 100.0%; Pred. No. 4,7e-158;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEQNSTDYEEENMGTYDYSQYELICKEDEVEFAKFLPVFLTIVFVIGLAGNS 60
DB 1 MLEQNSTDYEEENMGTYDYSQYELICKEDEVEFAKFLPVFLTIVFVIGLAGNS 60

QY 61 MVAIAYAYKKORTKIDYIILNLAVADLLFLTPFWANAVHGVWLGKIMCKITSALT 120
DB 61 MVAIAYAYKKORTKIDYIILNLAVADLLFLTPFWANAVHGVWLGKIMCKITSALT 120
QY 121 LNFVSGMOFLACISIDRYAVATKVPSSQSGVGPWCWICFCVMAAILLSIPOLVFYTVND 180
DB 121 LNFVSGMOFLACISIDRYAVATKVPSSQSGVGPWCWICFCVMAAILLSIPOLVFYTVND 180
QY 181 NARCIPIPRVIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKMPNIXISRLK 240
DB 181 NARCIPIPRVIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKMPNIXISRLK 240
QY 241 VLLTVIVIVITQLPYNIVKFCRAIDIIYSLITSCMSKRMIDAIQVTSIALFHSCLNP 300
DB 241 VLLTVIVIVITQLPYNIVKFCRAIDIIYSLITSCMSKRMIDAIQVTSIALFHSCLNP 300
QY 301 ILVFMGASFKNYVMKAKKYSWRRORSVEEFPDSGTEPTSTPSI 350
DB 301 ILVFMGASFKNYVMKAKKYSWRRORSVEEFPDSGTEPTSTPSI 350

RESULT 9

US-10-407-079-84
Sequence 84, Application US/10407079
Publication No. US20030215860A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Glucksmann, Maria A.
APPLICANT: Siles-Santiago, Imaculada
APPLICANT: Carroll, Joseph M.
APPLICANT: Galvin, Katherine M.
TITLE OF INVENTION: 45449, 52829, 52872 AND 26908 MOLECULES AND USES THEREFOR
FILE REFERENCE: MFI03-0510NM
CURRENT APPLICATION NUMBER: US/10/407,079
CURRENT FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: US 10/226,102
PRIOR FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/314,041
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 10/225,094
PRIOR FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: US 60/314,185
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 10/272,417
PRIOR FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 09/715,790
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: US 60/191,845
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 10/282,837
PRIOR FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US 09/796,338
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/186,059
PRIOR FILING DATE: 2000-02-29
REMAINING PRIOR APPLICATION data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 84
LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
US-10-407-079-84

Query Match 100.0%; Score 1819; DB 15; Length 350;
Best Local Similarity 100.0%; Pred. No. 4,7e-158;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEQNSTDYEEENMGTYDYSQYELICKEDEVEFAKFLPVFLTIVFVIGLAGNS 60
DB 1 MLEQNSTDYEEENMGTYDYSQYELICKEDEVEFAKFLPVFLTIVFVIGLAGNS 60


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QY      61  MVAIAYKKORTKTDVYIILNLAVALDLLFTLPMAVNAVHGVLGKIMCKITSALYT 120
Db      61  MVAIAYKKORTKTDVYIILNLAVALDLLFTLPMAVNAVHGVLGKIMCKITSALYT 120
QY      121  LNFVSGMOFLACISIDRYAVATKVPSSQGVGKPCWIIICVMAAAILISIPOLVFYTVND 180
Db      121  LNFVSGMOFLACISIDRYAVATKVPSSQGVGKPCWIIICVMAAAILISIPOLVFYTVND 180
QY      181  NARCIPFPRLYGTSKKALIQMLEICIGFVPPFLMGVCYFTTARTLMKMPNIKISRLPK 240
Db      181  NARCIPFPRLYGTSKKALIQMLEICIGFVPPFLMGVCYFTTARTLMKMPNIKISRLPK 240
QY      241  VLLTVVIVFIVTQLPYNIYVFCRAIDIIYSLITSCKMSKMDIAIQVTSIALFHSCLNIP 300
Db      241  VLLTVVIVFIVTQLPYNIYVFCRAIDIIYSLITSCKMSKMDIAIQVTSIALFHSCLNIP 300
QY      301  LLYFMGASFKNYVMKAKKYGSMRQROSVVEFPDSEGPTEPTSTFSI 350
Db      301  LLYFMGASFKNYVMKAKKYGSMRQROSVVEFPDSEGPTEPTSTFSI 350

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RESULT 10
US-09-765-994-4
; Sequence 4, Application US/09765994
; Patent No. US20010016336A1
; GENERAL INFORMATION:
; APPLICANT: ELLIS, CATHERINE
; TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: GH-70225-C1
; CURRENT APPLICATION NUMBER: US/09/765,994
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/055,895
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: 08/962,922
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 349
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-765-994-4

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Query Match      99.7%; Score 1814; DB 9; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.4e-157;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  ALEQNSTDYEEENENGTVDYSQYELCIKEDVREFAKVFLPVFLTIIVFVIGLAGNSM 61
Db      1  ALEQNSTDYEEENENGTVDYSQYELCIKEDVREFAKVFLPVFLTIIVFVIGLAGNSM 60
QY      62  VVAIAYKKORTKTDVYIILNLAVALDLLFTLPMAVNAVHGVLGKIMCKITSALYT 121
Db      61  VVAIAYKKORTKTDVYIILNLAVALDLLFTLPMAVNAVHGVLGKIMCKITSALYT 120
QY      122  NFNSGMOFLACISIDRYAVATKVPSSQGVGKPCWIIICVMAAAILISIPOLVFYTVND 181
Db      121  NFNSGMOFLACISIDRYAVATKVPSSQGVGKPCWIIICVMAAAILISIPOLVFYTVND 180
QY      182  ARCIPIFPRLYGTSKKALIQMLEICIGFVPPFLMGVCYFTTARTLMKMPNIKISRLPK 241
Db      181  ARCIPIFPRLYGTSKKALIQMLEICIGFVPPFLMGVCYFTTARTLMKMPNIKISRLPK 240
QY      241  LTVVIVFIVTQLPYNIYVFCRAIDIIYSLITSCKMSKMDIAIQVTSIALFHSCLNIP 301
Db      241  LTVVIVFIVTQLPYNIYVFCRAIDIIYSLITSCKMSKMDIAIQVTSIALFHSCLNIP 300
QY      302  LLYFMGASFKNYVMKAKKYGSMRQROSVVEFPDSEGPTEPTSTFSI 350
Db      301  LLYFMGASFKNYVMKAKKYGSMRQROSVVEFPDSEGPTEPTSTFSI 349

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RESULT 11
US-10-403-161-12
; Sequence 12, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: Cnaseqdist version 0.1
; SEQ ID NO 12
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-161-12

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Query Match      99.5%; Score 1810; DB 12; Length 348;
Best Local Similarity 100.0%; Pred. No. 3.1e-157;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  LEQNSTDYEEENENGTVDYSQYELCIKEDVREFAKVFLPVFLTIIVFVIGLAGNSM 62
Db      1  LEQNSTDYEEENENGTVDYSQYELCIKEDVREFAKVFLPVFLTIIVFVIGLAGNSM 60
QY      63  VVAIAYKKORTKTDVYIILNLAVALDLLFTLPMAVNAVHGVLGKIMCKITSALYT 122
Db      61  VVAIAYKKORTKTDVYIILNLAVALDLLFTLPMAVNAVHGVLGKIMCKITSALYT 120
QY      123  FVSGMOFLACISIDRYAVATKVPSSQGVGKPCWIIICVMAAAILISIPOLVFYTVND 182
Db      121  FVSGMOFLACISIDRYAVATKVPSSQGVGKPCWIIICVMAAAILISIPOLVFYTVND 180
QY      183  RCIPFPRLYGTSKKALIQMLEICIGFVPPFLMGVCYFTTARTLMKMPNIKISRLPK 242
Db      181  RCIPFPRLYGTSKKALIQMLEICIGFVPPFLMGVCYFTTARTLMKMPNIKISRLPK 240
QY      243  LTVVIVFIVTQLPYNIYVFCRAIDIIYSLITSCKMSKMDIAIQVTSIALFHSCLNIP 302
Db      241  LTVVIVFIVTQLPYNIYVFCRAIDIIYSLITSCKMSKMDIAIQVTSIALFHSCLNIP 300
QY      303  YVFMGASFKNYVMKAKKYGSMRQROSVVEFPDSEGPTEPTSTFSI 350
Db      301  YVFMGASFKNYVMKAKKYGSMRQROSVVEFPDSEGPTEPTSTFSI 348

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RESULT 12
US-10-272-983-22
; Sequence 22, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:

```

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; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huang T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-983-22

Query Match      99.5%; Score 1810; DB 14; Length 350;
Best Local Similarity 99.4%; Pred. No. 3.2e-157;
Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 M A L E O N O S T D Y Y E E N M N G T D Y S Q Y E L I C I K E D V R E F A K V L P F L T I V F I G L A G N S 60
DB      1 M A L E O N O S T D Y Y E E N M N G T D Y S Q Y E L I C I K E D V R E F A K V L P F L T I V F I G L A G N S 60
QY      61 M V A I A Y Y K K O R T K D V Y I L N L A V A D L L L F T L P F M A V N A V H G W L G K I M K I T S A L Y T 120
DB      61 M V A I A Y Y K K O R T K D V Y I L N L A V A D L L L F T L P F M A V N A V H G W L G K I M K I T S A L Y T 120
QY      121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C W I I C C V M M A A I L L S I P O L V F Y T V N D 180
DB      121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C W I I C C V M M A A I L L S I P O L V F Y T V N D 180
QY      181 N A R C I P F P R Y I G T S M K A L I Q M L E I C I G F V P F L M G V C Y F I T A R T L M K M P I K I S R P L K 240
DB      181 N A R C I P F P R Y I G T S M K A L I Q M L E I C I G F V P F L M G V C Y F I T A R T L M K M P I K I S R P L K 240
QY      241 V L L T V I V F I V T Q L P N I V K F C R A I D I I Y S L I T S C M S K R M D I A I Q V T E S I A L F H S C L N P 300
DB      241 V L L T V I V F I V T Q L P N I V K F C R A I D I I Y S L I T S C M S K R M D I A I Q V T E S I A L F H S C L N P 300
QY      301 I L V F E M G A S F K N Y V M K V A K K Y G S M R R O S V E E F P D S E G P T E P T S T S I 350
DB      301 I L V F E M G A S F K N Y V M K V A K K Y G S M R R O S V E E F P D S E G P T E P T S T S I 350

```

RESULT 13
US-10-393-807-22

; Sequence 22, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huang T.

```

; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-393-807-22

Query Match      99.5%; Score 1810; DB 14; Length 350;
Best Local Similarity 99.4%; Pred. No. 3.2e-157;
Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 M A L E O N O S T D Y Y E E N M N G T D Y S Q Y E L I C I K E D V R E F A K V L P F L T I V F I G L A G N S 60
DB      1 M A L E O N O S T D Y Y E E N M N G T D Y S Q Y E L I C I K E D V R E F A K V L P F L T I V F I G L A G N S 60
QY      61 M V A I A Y Y K K O R T K D V Y I L N L A V A D L L L F T L P F M A V N A V H G W L G K I M K I T S A L Y T 120
DB      61 M V A I A Y Y K K O R T K D V Y I L N L A V A D L L L F T L P F M A V N A V H G W L G K I M K I T S A L Y T 120
QY      121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C W I I C C V M M A A I L L S I P O L V F Y T V N D 180
DB      121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C W I I C C V M M A A I L L S I P O L V F Y T V N D 180
QY      181 N A R C I P F P R Y I G T S M K A L I Q M L E I C I G F V P F L M G V C Y F I T A R T L M K M P I K I S R P L K 240
DB      181 N A R C I P F P R Y I G T S M K A L I Q M L E I C I G F V P F L M G V C Y F I T A R T L M K M P I K I S R P L K 240
QY      241 V L L T V I V F I V T Q L P N I V K F C R A I D I I Y S L I T S C M S K R M D I A I Q V T E S I A L F H S C L N P 300
DB      241 V L L T V I V F I V T Q L P N I V K F C R A I D I I Y S L I T S C M S K R M D I A I Q V T E S I A L F H S C L N P 300
QY      301 I L V F E M G A S F K N Y V M K V A K K Y G S M R R O S V E E F P D S E G P T E P T S T S I 350
DB      301 I L V F E M G A S F K N Y V M K V A K K Y G S M R R O S V E E F P D S E G P T E P T S T S I 350

```

RESULT 14
US-10-417-820A-24

; Sequence 24, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.

APPLICANT: Behan, Dominic P.
 TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
 TITLE OF INVENTION: Receptors
 FILE REFERENCE: 7:US28,CON
 CURRENT APPLICATION NUMBER: US/10/417,820A
 CURRENT FILING DATE: 2003-04-16
 PRIOR APPLICATION NUMBER: 09/416,760
 PRIOR FILING DATE: 1999-10-12
 PRIOR APPLICATION NUMBER: 09/170,496
 PRIOR FILING DATE: 1998-10-13
 PRIOR APPLICATION NUMBER: 60/110,060
 PRIOR FILING DATE: 1998-11-27
 PRIOR APPLICATION NUMBER: 60/120,416
 PRIOR FILING DATE: 1999-02-16
 PRIOR APPLICATION NUMBER: 60/121,852
 PRIOR FILING DATE: 1999-02-26
 PRIOR APPLICATION NUMBER: 60/109,213
 PRIOR FILING DATE: 1998-11-20
 PRIOR APPLICATION NUMBER: 60/123,944
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,945
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,948
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,951
 PRIOR FILING DATE: 1999-03-12
 Remaining Prior Application data removed - See file Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 155
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 24
 LENGTH: 350
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-417-820A-24

Query Match 99.5%; Score 1810; DB 15; Length 350;
 Best Local Similarity 99.4%; Pred. No. 3.2e-157;
 Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	MALEQNSTDYEEENENNGTYDSQYELICIKEDVREFAKFLPVFLTIYFVIGLAGNS	60
DB	1	MALEQNSTDYEEENENNGTYDSQYELICIKEDVREFAKFLPVFLTIYFVIGLAGNS	60
QY	61	MVAIVAYVKKKRTKIDVYILNLAVADLLFTLPFAVAVAGWVGLKIMCKITSALYT	120
DB	61	MVAIVAYVKKKRTKIDVYILNLAVADLLFTLPFAVAVAGWVGLKIMCKITSALYT	120
QY	121	LNFSQMOFLACISIDRYAVATVPQSQGVGKPCWIIICFCVMAAILLSIPOLVFYTVND	180
DB	121	LNFSQMOFLACISIDRYAVATVPQSQGVGKPCWIIICFCVMAAILLSIPOLVFYTVND	180
QY	181	NARCIIPFRYLGSMKALIQMLEICIGFVPELIMGVCYFIARTLMKPNKISPLK	240
DB	181	NARCIIPFRYLGSMKALIQMLEICIGFVPELIMGVCYFIARTLMKPNKISPLK	240
QY	241	VLTIVIVFIVTQLPYNIYVFCRAIDIIYSLITSCNMSKMDIAIQVTSIALFHSCLNP	300
DB	241	VLTIVIVFIVTQLPYNIYVFCRAIDIIYSLITSCNMSKMDIAIQVTSIALFHSCLNP	300
QY	301	ILYVFMGASFKNYVMKAKKYGSRQROSVVEFPDSEPTSTFSI	350
DB	301	ILYVFMGASFKNYVMKAKKYGSRQROSVVEFPDSEPTSTFSI	350

RESULT 15
 US-09-910-695-8
 Sequence 8, Application US/09910695
 Publication No. US20030166052A1
 GENERAL INFORMATION:
 APPLICANT: Hedrick, Joseph A.
 Vicari, Alain P.
 Zlocnik, Albert
 TITLE OF INVENTION: Mammalian Chemokines; Receptors;

NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DMAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/910,695
 FILING DATE: 20-Jul-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/122,585
 FILING DATE: 24-Jul-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0757
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 852-9196
 TELEFAX: (650) 496-1200
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 350 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-09-910-695-8

Query Match 99.1%; Score 1803; DB 10; Length 350;
 Best Local Similarity 99.4%; Pred. No. 1.4e-156;
 Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	MALEQNSTDYEEENENNGTYDSQYELICIKEDVREFAKFLPVFLTIYFVIGLAGNS	60
DB	1	MALEQNSTDYEEENENNGTYDSQYELICIKEDVREFAKFLPVFLTIYFVIGLAGNS	60
QY	61	MVAIVAYVKKKRTKIDVYILNLAVADLLFTLPFAVAVAGWVGLKIMCKITSALYT	120
DB	61	MVAIVAYVKKKRTKIDVYILNLAVADLLFTLPFAVAVAGWVGLKIMCKITSALYT	120
QY	121	LNFSQMOFLACISIDRYAVATVPQSQGVGKPCWIIICFCVMAAILLSIPOLVFYTVND	180
DB	121	LNFSQMOFLACISIDRYAVATVPQSQGVGKPCWIIICFCVMAAILLSIPOLVFYTVND	180
QY	181	NARCIIPFRYLGSMKALIQMLEICIGFVPELIMGVCYFIARTLMKPNKISPLK	240
DB	181	NARCIIPFRYLGSMKALIQMLEICIGFVPELIMGVCYFIARTLMKPNKISPLK	240
QY	241	VLTIVIVFIVTQLPYNIYVFCRAIDIIYSLITSCNMSKMDIAIQVTSIALFHSCLNP	300
DB	241	VLTIVIVFIVTQLPYNIYVFCRAIDIIYSLITSCNMSKMDIAIQVTSIALFHSCLNP	300
QY	301	ILYVFMGASFKNYVMKAKKYGSRQROSVVEFPDSEPTSTFSI	350
DB	301	ILYVFMGASFKNYVMKAKKYGSRQROSVVEFPDSEPTSTFSI	350

Search completed: April 13, 2004, 13:20:10
 Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 13, 2004, 13:15:19 ; Search time 20 Seconds
(without alignments)
1683.352 Million cell updates/sec

Title: US-09-721-341-2

Perfect score: 1819
Sequence: 1 MALEONQSTDYEEENMNG.....VEEFPDSEGPTEPTSTFSI 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*

- 1: PIR1:*
- 2: PIR2:*
- 3: PIR3:*
- 4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1620	89.1	350	2 JN0621	G protein-coupled
2	659	36.2	378	2 B55735	lymphocyte-specific
3	650	35.7	378	2 A55735	G protein-coupled
4	643	35.3	378	2 A55735	G protein-coupled
5	583	32.1	369	2 UC5068	G protein-coupled
6	537.5	29.5	360	2 A57160	chemokine (C-C) re
7	534.5	29.4	360	2 A57160	interleukin-8 rece
8	524	28.8	354	2 I58186	probable G protein
9	522.5	28.7	355	2 UC4304	orphan G protein-c
10	522.5	28.7	360	2 UC4587	chemokine (C-C) re
11	518.5	28.5	354	2 B55735	G protein-coupled
12	511	28.1	358	2 A53752	interleukin-8 rece
13	501.5	27.6	355	2 JQ1231	interleukin-8 rece
14	500.5	27.5	352	2 A45747	neuropeptide Y/pep
15	499.5	27.5	353	2 S28787	neuropeptide Y/pep
16	493.5	27.1	352	2 G00048	chemokine (C-C) re
17	492	27.0	360	2 UC2443	chemokine (C-C) re
18	489.5	26.9	350	2 A39445	interleukin-8 rece
19	486	26.7	355	2 UC5067	G protein-coupled
20	485	26.7	355	2 A53739	macrophage inflamm
21	484.5	26.6	352	2 A43133	chemokine (C-C) re
22	483.5	26.6	359	2 A48921	interleukin-8 rece
23	482	26.5	374	2 I38450	chemokine (C-C) re
24	479.5	26.4	359	2 I49341	MMP-1 alpha recept
25	476.5	26.2	367	2 UC0349	interleukin-inducib
26	474	26.1	355	2 A45177	chemokine (C-C) re
27	471	25.9	356	2 S42036	interleukin-8 rece
28	470	25.8	383	2 S55594	G protein-coupled
29	461.5	25.4	355	2 G02436	chemokine (C-C) re

30	455.5	25.0	359	2 S44425	angiotensin II rec
31	452.5	24.9	359	2 UC1104	angiotensin II rec
32	452.5	24.9	359	2 UC2134	angiotensin II rec
33	450	24.7	359	2 S15403	angiotensin II rec
34	450	24.7	374	2 S32785	G protein-coupled
35	446.5	24.5	359	2 A48857	angiotensin II rec
36	445.5	24.5	356	2 I19340	MMP-1 alpha recept
37	442.5	24.3	372	2 S26667	G protein-coupled
38	442.5	24.3	374	2 S42628	G protein-coupled
39	441	24.2	362	2 JN0694	angiotensin II rec
40	439	24.1	359	2 A42656	angiotensin II rec
41	438.5	24.1	359	2 JN0621	angiotensin II rec
42	438.5	24.1	362	2 A39714	G protein-coupled
43	437.5	24.1	327	2 S56162	MDR1 protein - h
44	434	23.9	359	2 UC1516	angiotensin II rec
45	428.5	23.6	359	2 I39418	angiotensin II rec

ALIGNMENTS

RESULT 1

JN0621
G protein-coupled receptor type B - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000

C/Accession: JN0621

R/Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.

Biochem. Biophys. Res. Commun. 194, 504-511, 1993

A/Title: Identification of novel members of G-protein coupled receptor superfamily expres

A/Reference number: JN0621; MUID:93326166; PMID:8392843

A/Accession: JN0621

A/Molecule type: mRNA

A/Residues: 1-350 <MAT>

A/Cross-references: GB:863848; NID:9399710; PIDN:A4827547.1; PID:9399711

A/Experimental source: Tongue taste papillae

C/Comment: This protein is involved in modulating taste sensitivity or regeneration of t

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

F/80-99/Domain: transmembrane #status predicted <TM2>

F/114-135/Domain: transmembrane #status predicted <TM3>

F/154-175/Domain: transmembrane #status predicted <TM4>

F/200-222/Domain: transmembrane #status predicted <TM5>

F/242-265/Domain: transmembrane #status predicted <TM6>

F/284-306/Domain: transmembrane #status predicted <TM7>

F/6.19/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match

Best Local Similarity 89.1%; Score 1620; DB 2; Length 350;

Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY	1	MALEONQSTDYEEENMNGTDYQVELICKEQVREFAKFLVFPITIVIGLAGNS	60
DB	1	MAVEYNQSTDYEEENMNDTHDYSQYEVICKEVRFAKFLVFAFTINIIQLAGNS	60
QY	61	MYVAIYAYKKQRTKTDVYIINLAVADLLFTLPFAVNAVHGVNLGKIKITSAIYT	120
DB	61	TVAIYAYKKRRTKTDVYIINLAVADLLFTLPFAVNAVHGVNLGKIMCKVTSALYT	120
QY	121	LMFVSGMQLACISIDRYAAVTKVPSQSGVGRKCIIFECVMAAILISIPLVFYVND	180
DB	121	VNFVSGMQLACISIDRYAAVTKVPSQSGVGRKCIIFECVMAAILISIPLVFYVNH	180
QY	181	NARCIPFPFYLGTSKMLIQMLEICIGFVPEFLMGVCYFTTAPTLKMPENIKISRLK	240
DB	181	KARCPVFPFYHGTSMKASIQLEICIGFIIFPLIMAVCYFTTAKTLKMPINIKSQPLK	240
QY	241	VLLTVIVIVIVQLPNYIVKFCRAIDIIYSLTSCMKMKMDIAIQVESIALPFSCLNP	300
DB	241	VLFVTVIVIVIVQLPNYIVKFCQALDIISLTSCMSKRDVAIQIESIALPFSCLNP	300
QY	301	ILVFWGSAFKNYVWKVAKYGSNRRORSVEEFPDSEGPTEPTSTFSI	350

Db 301 VLVFNGTSPKRYIMVAKKYSGRQRQVNEIRPESDAPETSTFET 350

RESULT 2

lymphocyte-specific G protein-coupled receptor EB11 - human
B55735

N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1

C:Species: Homo sapiens (man)

C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000

C:Accession: B55735; S52443

R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B. Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor

A:Reference number: A55735; MUID:95154835; PMID:7851893

A:Accession: B55735

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-378 <SCH>

A:Cross-references: GB:L31581; NID:g468319; PIDN:AAA74231.1; PID:g468320

R:Burghalter, R.; Kempkes, B.; Staube, K.; Lipp, M.

Submitted to the EMBL Data Library, February 1995

A:Description: The expression of the chemokine receptor BLR2/EB11 is specifically trans

A:Reference number: S52443

A:Accession: S52443

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 21-378 <BUR>

A:Cross-references: EMBL:X84702

C:Genetics:

A:Gene: GDB:CMK87; EB11; BLR2; CCR7

A:Cross-references: GDB:342065; OMIM:600242

A:Map position: 17q12-17q21.2

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 36.2%; Score 659; DB 2; Length 378;

Best Local Similarity 38.7%; Pred. No. 4.9e-49;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEONSTDYEEENMGTYDYSOVELICIKEDVREPAKVLPEVLTIVFVIGLAGNS 60
DB 21 VCICQDEVTDDYIGDNT---TVDYTLFESICSKDVNFKAMFLPMYSIICFVGLGNG 77
QY 61 MVVAIYAYKKORTKDVYILNLAVADLLFTLPFMANAVHGVLGIMKIKISALYT 120
DB 78 LVVLTYIFRKLKMTDVTYLNLAVDLFLTLFPMAISAASWVGVHFKLLFATYK 137
QY 121 LNFVSGMQLACTSIDRYVAATKPS---QSGVGRPCWIIICVMAAILLSIPOLVY 176
DB 138 MSFSSGMLLLCTSIDRYVAIVQAVSAHRHARVLLISKLSGVGIWILATVLSIPELYS 197
QY 177 TVNDNA---RCIPFRVLGSMKALLQMEICIGFVFPFLIMGVCFITARTLMKMP 231
DB 198 DLRRSSSEQMRQSLTHER--VEAFITQVAAQVIGFVPLPAMSFCVLIIRTLQAR 254
QY 232 NIKISREPLKYLTVIVFIVTQLPYNIYKFCRAIDIIYSLITSNNKSKMDIAIQYTES 291
DB 255 NPEKNKAIKYIIVAVVFIVFQLPYNGVLAQTVANFNITSSCELSKQLNIAVDYTSL 314
QY 292 ALFHSCINPLIYFMGASFKNYMKYAKKYG-----SW-----RQROSVVEFPD 337
DB 315 ACVRCCNPLVAFIVGKFRNDLFKFLKDGCLSQERLRHMSSCRHRRSSMSVE---- 369
QY 338 SEGTPTSTSTFS 349
DB 370 ---AETTTFS 377

RESULT 3

G protein-coupled receptor EB11 - mouse

A55735

C:Species: Mus musculus (house mouse)

C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999

C:Accession: A55735

R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B. Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor

A:Reference number: A55735; MUID:95154835; PMID:7851893

A:Accession: A55735

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-378 <SCH>

A:Cross-references: GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g468341

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 35.7%; Score 650; DB 2; Length 378;

Best Local Similarity 38.3%; Pred. No. 2.9e-48;

Matches 140; Conservative 67; Mismatches 125; Indels 34; Gaps 8;

QY 5 QNSTDYEEENMGTYDYSOVELICIKEDVREPAKVLPEVLTIVFVIGLAGNSVVA 64
DB 25 QDEVTDDYIGDNT---TVDYTLFESICSKDVNFKAMFLPMYSIICFVGLGNGLVIL 81
QY 65 IYAYKKORTKDVYILNLAVADLLFTLPFMANAVHGVLGIMKIKITSAIYTLNFV 124
DB 82 TYIFRKLKMTDVTYLNLAVDLFLTLFPMAISAASWVGVHFKLLFATYKLSF 141
QY 125 SGMQFLACTSIDRYVAATKPSQSG-----VGRPCWIIICVMAAILLSIPOLVYT 177
DB 142 SGMILLCTSIDRYVAIVQAVSAHRHARVLLISK--LSCVGIWILATVLSIPELIYSG 198
QY 178 VNDA---RCIPFRVLGSMKALLQMEICIGFVFPFLIMGVCFITARTLMKMP 230
DB 199 LQKNSGEDTLK---SLVSAQVEALITQVAAQVIGFVPLPAMSFCVLIIRTLQAR 253
QY 231 NIKISREPLKYLTVIVFIVTQLPYNIYKFCRAIDIIYSLITSNNKSKMDIAIQYTES 290
DB 254 NPEKNKAIKYIIVAVVFIVFQLPYNGVLAQTVANFNITSSCELSKQLNIAVDYTS 313
QY 291 IALFHSCINPLIYFMGASFKNYMKYAKKYSRRR-----QSVVEFPDSEPT 343
DB 314 LASVRCCNPLVAFIVGKFRSDLFKFLKDGCLSQERLRHMSSCRHRRSSMSVMB--AE 371
QY 344 PTSTFS 349
DB 372 TTTTFS 377

RESULT 4

G protein-coupled peptide receptor EB1 1 - human

C:Species: Homo sapiens (man)

C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999

C:Accession: A45680

R:Bitkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E. J. Virol. 67, 2209-2220, 1993

A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled p

A:Reference number: A45680; MUID:93189173; PMID:8353238

A:Accession: A45680

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-378 <BB>

A:Cross-references: GB:L08176; NID:g183484; PID:g183485

A:Experimental source: B-lymphocytes

A:Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBI:127095)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 35.3%; Score 643; DB 2; Length 378;

Best Local Similarity 39.0%; Pred. No. 1.2e-47;

Matches 145; Conservative 62; Mismatches 127; Indels 38; Gaps 8;

QY 1 MALEONSTDYEEENMGTYDYSOVELICIKEDVREPAKVLPEVLTIVFVIGLAGNS 60
DB 21 VCICQDEVTDDYIGDNT---TVDYTLFESICSKDVNFKAMFLPMYSIICFVGLGNG 77

Db 21 VCLQCEVTDYDYGNT--TVDYTLFESLCSKDVNFKAMFLPMYSIICFVGLGNG 77

Qy 61 MVAIAIYVYKQRTKDVYILNLAVALDLLFTLPFWANAVAGWLGKIMCKITSAIYT 120

Db 78 LVVLTITVFRLKTMVDYILNLAVALDLLFTLPFWANAVAGWLGKIMCKITSAIYT 137

Qy 121 LNVSGMOPACISIDRYAVAVTKVPSQSGVGRKCMII--CFQYMAA--ALLISIPOLVY 176

Db 138 MSFSGGLLLLCISIDRYAVAVTKVPSQSGVGRKCMII--CFQYMAA--ALLISIPOLVY 197

Qy 177 TVNDNA-----RCIPFRYLGTSKALIQMLEICIGFVFPFLMGVCYFITARLTKMP 231

Db 198 DLGRSSSEQMRCSLIEH---VEAFITIQVAGMVGFLVPLLMGFCVLIIIRTLQAR 254

Qy 232 NITISRLKLVLTAVVIVITQLPYNIKFCRAIDIIYSITSCNMSKMDIAIQVTEI 291

Db 255 NFRNKAKIVIAVAVVIVITQLPYNIKFCRAIDIIYSITSCNMSKMDIAIQVTEI 314

Qy 292 ALFHSCLNPLIYFMGASFKNYVMKAKKYG-----SM-----RROSGVSEFPED 337

Db 315 ACVRCNPLIYAFIGKFRNDLFLKFDGLGCLSGQLQKQSSCRHRSMSVY----- 369

Qy 338 SEGPTEPTSTFS 349

Db 370 ----AETTTTFS 377

RESULT 5

UCS068
G:Protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C>Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #ext_change 21-Jul-2000
C/Accession: JCS068

Rizbaillos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-like G
A:Reference number: JCS067, MUID:97040707, PMID:8886020
A/Accession: JCS068
A:Molecule type: DNA
A:Residues: 1-369 <ZB>
A:Cross-references: EMBL:Z79784, NID:g1668737, PIRN:CA802144.1, PID:g1668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C/Genetics:
A:Gene: GGB:CKMR6, STRL22, GPR29, CCR6, CKR-L3, GPR-CY4
A:Cross-references: GDB:5370639, OMIM:601835
A:Map position: 6q27-6q27
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-66/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 32.1%; Score 583; DB 2; Length 369;
Best Local Similarity 36.1%; Pred. No. 1.6e-42;
Matches 121; Conservative 68; Mismatches 120; Indels 26; Gaps 7;

Qy 8 STDYVYENEMNGYDYQYELICIKEDVREPAKVFPEFLTIVFVIGLAGNSMVAIYAY 67

Db 18 NTSIYSVDSSE-----LCSLOEVARQFSRLVPIYSICVFGLLGNLIVITTA 67

Qy 68 YXXKQRTKDVYILNLAVALDLLFTLPFWANAVAGWLGKIMCKITSAIYTINLVSG 126

Db 68 FYKARSMETVYILNLAVALDLLFTLPFWANAVAGWLGKIMCKITSAIYTINLVSG 127

Qy 127 MQLVACISIDRYAVAVTKVPSQSGVGRKCMII--CFQYMAA--ALLISIPOLVY 179

Db 128 MLVLTITVRLKTMVDYILNLAVALDLLFTLPFWANAVAGWLGKIMCKITSAIYTINLVSG 187

Qy 180 DNACIPFPYLGTS---MKALIQMLEICIGFVFPFLMGVCYFITARLTKMPENIKI 235

Db 188 GSDVC---EPKQGVSEIRKMLMLGLELFGFIFLMETIFCYTIVKTLVQAQNSKR 244

Qy 236 SRPLKLVLTAVVIVITQLPYNIKFCRAIDIIYSITSCNMSKMDIAIQVTEI 295

Db 245 HKARVIAVAVVITQLPYNIKFCRAIDIIYSITSCNMSKMDIAIQVTEI 303

Qy 296 SCNLPIYFMGASFKNYVMKAKKYG-----SM-----RROSGVSEFPED 330

Db 304 CCLNPVLYAFIGKFRNDLFLKFDGLGCLSGQLQKQSSCRHRSMSVY----- 338

RESULT 6

AS7160
Chemokine (C-C) receptor 4 - human
N/Alternate names: C-C CKR-4
C:Species: Homo sapiens (man)
C>Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #ext_change 21-Jul-2000
C/Accession: AS7160

R.Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; We
J.Biol. Chem. 270, 19495-19500, 1995
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDN
A:Reference number: AS7160, MUID:95370289, PMID:7642634
A/Accession: AS7160
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-360 <POW>
A:Cross-references: GB:X85740, NID:g1370103, PIRN:CA85743.1, PID:g971452
A/Note: source clone K5-5
C/Genetics:
A:Gene: GDB:CKMR4
A:Cross-references: GDB:677463
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
F:40-65/Domain: transmembrane #status predicted <TM1>
F:76-97/Domain: transmembrane #status predicted <TM2>
F:112-133/Domain: transmembrane #status predicted <TM3>
F:151-175/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:243-264/Domain: transmembrane #status predicted <TM6>
F:291-308/Domain: transmembrane #status predicted <TM7>
F:29-276/110-187/Disulfide bonds: #status predicted
F:72-350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:183/194/Binding site: carboxylate (Asn) (covalent) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 29.5%; Score 537.5; DB 2; Length 360;
Best Local Similarity 35.8%; Pred. No. 1.3e-38;
Matches 115; Conservative 63; Mismatches 124; Indels 19; Gaps 6;

Qy 10 DYVEENEMNGYDYQYELICIKEDVREPAKVFPEFLTIVFVIGLAGNSMVAIYAY 69

Db 8 DTTDESISNVYIYES-PRKCTKEGIVAFGLFLPPLYSIVFVFGLLGNLIVITTA 67

Qy 70 KKQRTKDVYILNLAVALDLLFTLPFWANAVAGWLGKIMCKITSAIYTINLVSG 129

Db 68 KRLRSMETVYILNLAVALDLLFTLPFWANAVAGWLGKIMCKITSAIYTINLVSG 127

Qy 130 LACISIDRYAVAVTKVPSQSGVGRKCMII--CFQYMAA--ALLISIPOLVY 179

Db 128 VMLMSIDRYAVAVTKVPSQSGVGRKCMII--CFQYMAA--ALLISIPOLVY 182

Qy 180 DNACIPFPYLGTS---MKALIQMLEICIGFVFPFLMGVCYFITARLTKMPENIKI 238

Db 183 NHTYKITYS--INSTWQVSSLEINILGIVPGLMFCYSMTIRLQCKNEKXKA 240

Qy 239 LKVLTVIVITQLPYNIKFCRAIDIIYSITSCNMSKMDIAIQVTEI 298

Db 241 VKMIAVAVVITQLPYNIKFCRAIDIIYSITSCNMSKMDIAIQVTEI 303

Qy 299 NPIYFMGASFKNYVMKAKKYG-----SM-----RROSGVSEFPED 339

A:Experimental source: peripheral blood mononuclear cell
 C:Comment: This protein is a cell-surface receptor which recognizes extracellular signal
 C:Comment: This protein is a key regulator of many immune and homeostatic responses, and
 C:Genetics:
 A:Gene: v28
 A:Map position: 3pter-p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
 F/35-57/Domain: transmembrane #status predicted <TM1>
 F/66-88/Domain: transmembrane #status predicted <TM2>
 F/104-125/Domain: transmembrane #status predicted <TM3>
 F/146-165/Domain: transmembrane #status predicted <TM4>
 F/197-217/Domain: transmembrane #status predicted <TM5>
 F/230-254/Domain: transmembrane #status predicted <TM6>
 F/275-296/Domain: transmembrane #status predicted <TM7>

Query Match 28.7%; Score 522.5; DB 2; Length 355;
 Best Local Similarity 36.4%; Pred. No. 2.4e-37;
 Matches 112; Conservative 57; Mismatches 122; Indels 17; Gaps 5;

QY 22 YDYSQVELLCKEYREFAKFLPVFLTIYVIGLAGNSVVAIYAYKKQRTQTVYLL 81
 DB 12 FEYDIAEACVIGIVGFVIFSVFALGVNLLVFPALTNKKPKSVTDIYLL 71
 QY 82 NLAVADLLFTLPFMAVNAHGVLGKIMCKITSALTINFSGMQFLACISIDRYVAV 141
 DB 72 NLALSDLLFVALTPFWTHYLINKEGLNACKETTAFPIFGFSGIFFTIVISIDRYLAI 131
 QY 142 TKYPS-----QSGVKPCWIIICFCVMAAILLSIPQLVFYVNDNARCIPIPRYLGT 194
 DB 132 VLAANSNNNTVHGV-----TSLGWMAAILVAAPQFETIQKKN-ECLADYPEVLDS 185
 QY 195 SMKALIMELICIGFVVPFLIMGVCFITARTLMKNMNIISRLKVLTLVTVVFTQL 254
 DB 186 IMVPLAVRNVNPLGFLPLIMSYCFIRIQTLPSCNKKAKAILLILVAVFLPMT 245
 QY 255 PYNIVKFCRAIDIIYSILTSCKNSKRMDAIQVTESIALFHSCLNPILYVFMGSPKNYV 314
 DB 246 PYNMIFLETLK-LYDFPFCDMRKDIRLALSVETEVAFSHCCLNPLIYVAFAEKERRYL 304
 QY 315 MKYAKKYG 322
 DB 305 YHL---YG 309

RESULT 10
 JC4587

C:Chemokine (C-C) receptor 4 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
 C/Accession: JC4587
 R/Hoogwerf, A.U.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996
 A>Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
 A:Reference number: JC4587; MIMD:96136324; PMID:8573357
 A/Accession: JC4587
 A:Molecule type: mRNA
 A:Residues: 1-360 <HO>
 A/Cross-references: EMBL:X90862; NID:G1167851; PIDN:CA62372.1; PID:G1167852
 A:Experimental source: thymus
 C:Genetics:
 A:Gene: cc ckr-4
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: glycoprotein; phosphoprotein; receptor; thymus
 F/2183-194/Binding site: carboxylate (Asn) (covalent) #status predicted
 F/72-202/350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
 F/145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F/321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 28.7%; Score 522.5; DB 2; Length 360;
 Best Local Similarity 33.7%; Pred. No. 2.5e-37;
 Matches 110; Conservative 69; Mismatches 128; Indels 19; Gaps 6;

QY 3 LEONSTDYVEENENGTIDYSQVELLICKEDVREPAKFLPVFLTIYVIGLAGNSV 62
 DB 1 NMATEVTDITQDEITYNNGYFESMPKCTKEDGIAFBEVFLPYLSVFLGLFGNSV 60
 QY 63 VAIYAYKKQRTQTVYLLINAVADLLFTLPFMAVNAHGVLGKIMCKITSALTIN 122
 DB 61 VLVLFKRYRLKSMITVYLLINLAISDLFVLSLPFGVYAAQWFGDGLCKIVSMWYLVG 120
 QY 123 FVSGMQFLACISIDRYVAVTKV-----PSOSGVKPCWIIICFCVMAAILLSIPQLVF 175
 DB 121 FVSGIFLIMSIDRYLVAIVAVESLKRITLYGV-----ITSLITNSVAVPASLGLIF 175
 QY 176 ---YVNDNARCIPIPRYLGTSMKALIQMELI-CIGVVPFLIMGVCFITARTLMKP 231
 DB 176 STCYEHNHYCKIQYS--VNSTWKVLSLEINVLGLIPLIGIMLFYMSMIRTLQCK 233
 QY 232 NIKIRPFLKVLTLVTVVFTQLPYNIKFCRAIDIIYSILTSCKNSKRMDAIQVTESI 291
 DB 234 NEKRRARAMIFGVVPLGFWTPINVLFTETL-VELLEVLDCTLERKYLDAIQATETL 292
 QY 292 ALFHSCLNPILYVFMGSPKNYMKV 317
 DB 293 GRHSCCLNPVLYFPGERKRYITQL 318

RESULT 11
 B57733

G protein-coupled receptor GPR2 - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 26-Aug-1999
 C/Accession: B57733
 R/Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui, L.
 Genomics 23, 609-618, 1994
 A>Title: Cloning of human genes encoding novel G protein-coupled receptors.
 A:Reference number: B57733; MIMD:95154831; PMID:7851889
 A/Accession: B57733
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-354 <MAR>
 A/Cross-references: GB:U13667
 C:Genetics:
 A:Gene: GDB:GPR2
 A/Cross-references: GDB:371708; OMIM:600240
 A:Map position: 17q21.1-17q21.3
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor

Query Match 28.5%; Score 518.5; DB 2; Length 354;
 Best Local Similarity 33.9%; Pred. No. 5.4e-37;
 Matches 121; Conservative 65; Mismatches 142; Indels 29; Gaps 7;

QY 12 YVEENMGTDYSQVELLICKEDVREPAKFLPVFLTIYVIGLAGNSVVAIYAYK 70
 DB 5 HYSGDV-EDVSAAPLPELCKADYQAFSPQSVSLVAALGAGVLAHTLAAR 63
 QY 71 KQRTQTVYLLINAVADLLFTLPFMAVNAHGVLGKIMCKITSALTINFSGMQFL 130
 DB 64 AARSPTSAHLQLALADLLALTLPFAAGALQMSLSGSAICRTISGLYSASFHAGFL 123
 QY 131 ACISIDRYVAVTKV-----PSOSGVKPCWIIICFCVMAAILLSIPQLVFYVND--NAR 183
 DB 124 ACISADRYVAVTKVLPAGRPSTPGR-AHLVSVYVWLSLALFALLFSGDGGREGQR 182
 QY 184 CIPFPRYLGTSMKALIQMELICIGFVVPFLIMGVCFITARTLMKNPKIRISPLKVL 243
 DB 183 CRLIFPBGILQTVGAGAVQVALGFPALPIGWAVACVALLGRTLLARGERRALLRVV 242
 QY 244 TVVAVFTQLPYNIKFCRAIDIIYSILTSCKNSKRMDAIQVTESIALFHSCLNPI 303
 DB 243 ALVAVFVLLQPLVSLALLDITADLLARERSCPASKKDVALLVTSGLALARCGLNVL 302
 QY 304 VFMGSPKNYMKVAK-----KYGSWRORQSVVEFPDSEGTPTSTFSI 350

Db 303 AAFGLFRDRLRLRGSSPSGQPRRCGPRRLS-----SCSAPETHTSL 350

RESULT 12

A53752

Interleukin-8 receptor (clone 5B1a) - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #ext_change 05-Nov-1999

C/Accession: A53752

R/Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarro, J. Biol. Chem. 269, 12391-12394, 1994

A/Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.

A/Reference number: A53752; MUID:94220294; PMID:8175642

A/Accession: A53752

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-358 <PRA>

A/Cross-references: GB:L24445; NID:9437661; PIDN:AAA1378.1; PID:9437662

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 28.1%; Score 511; DB 2; Length 358;

Best Local Similarity 32.3%; Pred. No. 2,4e-36;

Matches 116; Conservative 72; Mismatches 139; Indels 32; Gaps 8;

Qy 10 DYVEENEMNGTYDYGQYELI-----CIKEDVREFAKFLPVFLTIVFVIGLA 57

Db 8 NYEYE--DFEG--DFSNYSYSIDLPPTLDSAPCRSESLTNSYVLIRYI-LVLESLIL 62

Qy 58 GNSMVAIAIAYKKQRTKTDVYLNLAVADLLFLTPFWAVNAHGVNLGKINCKITSA 117

Db 63 GNSLVMVLILYSRSTCSVDVYLLNLAIADLLFATLPTMAASKVHGWTFGTPLCKVSL 122

Qy 118 LVTLNFSVGQFPCISIDRYAVV-----TKVPSQSGVGKPCWIIICFCVMAAILLSIPQ 172

Db 123 VKENVYSGILLACISVDRIYLAIVHATRMIOKRLIVK----FICLSMGVSLLSLPI 178

Qy 173 LVEFYVNDNARCIPFPRYLGTS--MKALIQMLEICIGFVAVFLMGVCYFTARTIMK 229

Db 179 LLERNAIFPNSPVCEDMDGNSTAKRMVRLILPQTFGFIPLVLMLECYVFTLRTLFQ 238

Qy 230 MPRIKSRPLKVLTVIVIVIVQLPYNIVKPCRAIDIIYSLTSCNMSKMDIAIQVTE 289

Db 239 AHMGQGRARAVLFAVALLFLCLWLPYNVLVLTDTIMRTHVIOETERNDDIRLDATE 298

Qy 290 SIALLFHSCLNPILYVFMGASFKNYKVMKAKYGSWRCQ--ROSVEEPFDESGTEPT 345

Db 299 ILGLFHSCLNPIIYAFIQGFYGLKILAAHGLIKERFLAKESRPSFVASSSGNTSTT 357

RESULT 13

JQ1231

Interleukin-8 receptor - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #ext_change 05-Nov-1999

C/Accession: JQ1231; A46483

R/Beckmann, M.P.; Munger, W.E.; Kozlowsky, C.; Vandenbos, T.; Price, V.; Lyman, S.; Gerard Biochem. Biophys. Res. Commun. 179, 784-789, 1991

A/Title: Molecular characterization of the interleukin-8 receptor.

A/Reference number: JQ1231; MUID:91378994; PMID:1898400

A/Accession: JQ1231

A/Molecule type: DNA

A/Residues: 1-355 <BEC>

A/Cross-references: GB:M74240; NID:9165438; PIDN:AAA1375.1; PID:9165439

R/Dee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.

J. Immunol. 148, 1261-1264, 1992

A/Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.

A/Reference number: A46483; MUID:92148149; PMID:1737938

A/Accession: A46483

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-355 <BSE>

A/Cross-references: GB:M82873; NID:9165440; PIDN:AAA1376.1; PID:9165441

A/Experimental source: neutrophils

A/Note: sequence extracted from NCBI backbone (NCBI:81526, NCBI:81530)

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.6%; Score 501.5; DB 2; Length 355;

Best Local Similarity 33.1%; Pred. No. 1.5e-35;

Matches 107; Conservative 70; Mismatches 127; Indels 19; Gaps 6;

Qy 12 YVEENEMNGT-----YDYGQYELICIKEDVREFAKFLPVFLTIVFVIGLAGNSMVAI 65

Db 14 WFEDEFANAGMPFVEKDS--PCLVYTQTLNKVYV--VIVAVFLSLILGNSLMLV 68

Qy 66 YAYKKQRTKTDVYIINLAVADLLFLTPFWAVNAHGVNLGKINCKITSAIYTLNFS 125

Db 69 ILSRSNRSVTDVYLLNLAVADLLFALTWETMAVSKEKGIPTPLCKVSLKEVNFVS 128

Qy 126 GMQFLACISIDRYAVV--TKVPSQSGVGKPCWIIICFCVMAAILLSIPQVLYVNDNA 182

Db 129 GILLACISVDRIYLAIVHATRTLTQK--RLVVFICIGVIALSLILSPFLFRQVSPN 186

Qy 183 RCLIFPRYIG---TSKALIQMLEICIGFVAVFLMGVCYFTARTIMKPRIKSRPL 239

Db 187 NSSPVCYEDDGHNTAKRMVRLILPHTFGFIPLVLMLECYGFTLRTLFQAHMGQGRAM 246

Qy 240 KVLTVIVIVIVIVQLPYNIVKPCRAIDIIYSLTSCNMSKMDIAIQVTEISALFHSCLN 299

Db 247 RVIAVAVLIFLCPLPYNVLVLTDTIMRTHVIOETCORRDIRLDATEILGLFHSCLN 306

Qy 300 PIIYVFMGASFKNYKVMKAKYK 322

Db 307 PIIYAFIGONFRNGFLMLAARG 329

RESULT 14

A45747

Neuropeptide Y/receptor Y3 - human

N/Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor YESTR; re

C/Species: Homo sapiens (man)

C/Date: 03-May-1994 #sequence_revision 03-May-1994 #ext_change 05-Nov-1999

C/Accession: A45747; A53103; I53006; I59444; I69203; S32761

R/Federerpiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schuppert, K.; Clark-Lewis Genomica 16, 707-712, 1993

A/Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a pu

A/Reference number: A45747; MUID:93315164; PMID:8325644

A/Accession: A45747

A/Molecule type: mRNA

A/Residues: 1-352 <FRD>

A/Cross-references: GB:M99293; NID:9292516; PIDN:AAA16617.1; PID:9292517

R/Loetscher, M.; Geisler, T.; O'Reilly, T.; Zwaalen, R.; Baggiolini, M.; Noser, B. J. Biol. Chem. 269, 232-237, 1994

A/Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly e

A/Reference number: A53103; MUID:94103215; PMID:8276799

A/Accession: A53103

A/Molecule type: mRNA

A/Residues: 1-352 <LOB>

A/Cross-references: EMBL:X17635; NID:9297099; PIDN:CAA50641.1; PID:9297100

R/Herzog, H.; Horv, J.; Shine, J.; Seible, L.A. DNA Cell Biol. 12, 465-471, 1993

A/Title: Molecular cloning, characterization, and localization of the human homolog to t

A/Reference number: I53006; MUID:93319629; PMID:8329116

A/Accession: I53006

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: mRNA

A/Residues: 1-352 <HER>

A/Cross-references: GB:J06797; NID:9414929; PIDN:AAA03209.1; PID:9414928

R/Jaatin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salton, J.; Lar Regu. Pept. 47, 247-258, 1993

A/Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homolo

A/Reference number: I59444; MUID:9405833; PMID:824905

A/Accession: I59444

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: mRNA

A:Residues: 1-352 <R22>
 A:Cross-references: GB:L01639; NID:G189313; PID:AAA16594.1; PID:G189314
 Int. Immunol. 5, 1239-1249, 1993
 A:Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chem
 A:Reference number: 154751; MUID:94092629; PMID:7505609
 A:Accession: 169203
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-352 <R25>
 A:Cross-references: GB:D10924; NID:G219866; PID:BAH01722.1; PID:G219869
 C:Genetics:
 A:Gene: GDB:NPY3R; NPY3
 A:Cross-references: GDB:230002; OMIM:162643
 A:Map position: 2q21-2q21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.5%; Score 500.5; DB 2; Length 352;
 Best Local Similarity 34.6%; Pred. No. 1.9e-35;
 Matches 107; Conservative 57; Mismatches 134; Indels 11; Gaps 4;

QY 8 STDYVEENNGTYDYSQYELICIKEDVEFAKVPFLVFLTVFVGLAGNMAIYA 67
 Db 8 TSDNYTEE--MGSGDYDSMKKEPCFRENNANFNKIFLPTYSIIPLGIVNGVLVW 64
 QY 68 YKKQRTKTDVYIINLAVADLLFLTPFAVAVNAGVGLGKIMCKITSALYTLNFG 127
 Db 65 YQKLRMTKRYRLHLSVADLLFLVTLTPFAVAVNAGVGLGKAVHYTVNLVSSV 124
 QY 128 QPLACTSIDRYVAVTKPSQSGVKPC--WICFCVMAAILISIPOLVFYTV--NDNA 182
 Db 125 LILAFISLDYRLVAVHATNSQRPKLAEKVYVGVWIPALTLTPDFIFANVSEADRY 184
 QY 183 RCLPFPRIYIGTSMKALIQLEICIGFVFPFLMGVCYFTARTLMKPNIKISRLKVL 242
 Db 185 ICRFPFNDLMV--VVFQFOHIVGILPLGIVILSCYCIISKLSHSGVQKRAKLT 241
 QY 243 LTVVFIIVTQLPYNIKFCRAIDIIYSLITSCNMSKMDIAQVETESIALPFSCLNPL 302
 Db 242 VILILAFKACWLPYIGISIDSLILBETIKGCEPENTVHKMISTEALAFHCCINPL 301
 QY 303 YVFGASFK 311
 Db 302 YAFLGAKFK 310

RESULT 15

S28787
 neuropeptide Y/peptide YY receptor Y3 - bovine
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999
 C/Accession: S28787
 R:Rimland, J.; Xin, W.; Sweetnam, P.; Saijoh, K.; Nestler, E.J.; Duman, R.S.
 Mol. Pharmacol. 40, 869-875, 1991
 A:Title: Sequence and expression of a neuropeptide Y receptor cDNA.
 A:Reference number: S28787; MUID:92100053; PMID:1661837
 A:Accession: S28787
 A:Molecule type: mRNA
 A:Residues: 1-353 <RIM>
 A:Cross-references: EMBL:M86739
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 27.5%; Score 499.5; DB 2; Length 353;
 Best Local Similarity 34.5%; Pred. No. 2.3e-35;

Matches 106; Conservative 60; Mismatches 126; Indels 15; Gaps 5;

QY 13 YEENNGTYDYSQYELICIKEDVEFAKVPFLVFLTVFVGLAGNMAIYAYKKQ 72
 Db 12 YTEDDL-GSGDDYSMKKEPCFRENNANFNKIFLPTYSIIPLGIVNGVLVWGYQKRL 70
 QY 73 RRTKDVYIINLAVADLLFLTPFAVAVNAGVGLGKIMCKITSALYTLNFGVSGQFLAC 132

Db 71 RSNITDKRLHLSVADLLFLTPFAVAVNAGVGLGKAVHYTVNLVSSVLILAF 130
 QY 133 ISIDRYVAVTKPSQSGVKPC----WICFCVMAAILISIPOLVF---YTVNDNARC 184
 Db 131 ISLDRYLAVHATNSQ--KPKRLAEKVYVGVWLPVALLTLPDLIRADIKEDVERIYC 187
 QY 185 IPIFRYLOTSKALIQLEICIGFVFPFLMGVCYFTARTLMKPNIKISRLKVLIT 244
 Db 188 DRFPYSDL--MLVFQFOHIVGILPLGIVILSCYCIISKLSHSGVQKRAKLT 244
 QY 245 VIVFIVTQLPYNIKFCRAIDIIYSLITSCNMSKMDIAQVETESIALPFSCLNPLIYV 304
 Db 245 LITTFKACWLPYIGISIDSLILBETIKGCEPENTVHKMISTEALAFHCCINPLIYA 304
 QY 305 FVFGASFK 311
 Db 305 FLGAKFK 311

Search completed: April 13, 2004, 13:18:36
 Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 13, 2004, 13:15:19 ; Search time 18 seconds

(without alignments)
1012.475 Million cell updates/sec

Title: US-09-721-341-2

Sequence: 1 MAFQNDSTYYEENANG.....VEEPFDSGPEPTSTFSI 350

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1819	100.0	350	1	CKRB_HUMAN
2	1620	89.1	350	1	CKRB_BOVIN
3	659	36.2	378	1	CKR7_HUMAN
4	650	35.7	378	1	CKR7_MOUSE
5	639	35.1	369	1	CKR9_MOUSE
6	637	35.0	357	1	CKR9_HUMAN
7	605	33.3	367	1	CKR6_MOUSE
8	583	32.1	374	1	CKR6_HUMAN
9	581	31.9	342	1	CKR6_CERAE
10	571	31.4	342	1	CKR6_MACMU
11	569	31.3	342	1	CKR6_MACNE
12	566	31.1	343	1	CKR6_MACFA
13	560	30.8	342	1	CKR6_HUMAN
14	559	30.7	342	1	CKR6_PANTR
15	537.5	29.5	360	1	CKR4_HUMAN
16	534.5	29.4	360	1	IL6B_HUMAN
17	529.5	29.1	360	1	IL6B_HUMAN
18	527	29.0	364	1	CKB_PANTR
19	525	28.9	362	1	CKRA_HUMAN
20	524	28.8	354	1	IL6B_GORGO
21	522.5	28.7	353	1	IL6B_GORGO
22	522.5	28.7	355	1	CKX1_HUMAN
23	522.5	28.7	353	1	CKR4_MOUSE
24	521.5	28.7	353	1	IL6B_MOUSE
25	520.5	28.6	352	1	CKR4_MOUSE
26	512	28.1	356	1	IL6B_CANFA
27	511	28.1	354	1	CKX1_MOUSE
28	511	28.1	358	1	IL6B_PABIT
29	504	27.7	360	1	CKR2_MACMU
30	501.5	27.6	355	1	IL6B_PABIT
31	501.5	27.6	358	1	CKR3_CAVPO
32	500.5	27.5	352	1	CKR4_HUMAN
33	499.5	27.5	353	1	CKR4_BOVIN

34	499.5	27.5	360	1	IL6B_BOVIN	Q28003	bos taurus
35	498.5	27.4	352	1	CCR4_PAPAN	P56491	papio anubi
36	498.5	27.4	352	1	CCR5_CERPO	O62743	cercocebus
37	498.5	27.4	353	1	CCR4_FELCA	P56498	felis silve
38	497.5	27.4	350	1	IL6B_GORGO	P55919	gorilla gor
39	495.5	27.2	352	1	CCR5_CERAE	O62747	cercocebus
40	494.5	27.2	352	1	CCR4_CERPO	O62747	cercocebus
41	493.5	27.1	352	1	CCR4_MACFA	O28474	macaca fasc
42	493.5	27.1	352	1	CCR4_MACMU	P79394	macaca mula
43	492.5	27.1	359	1	CKR3_PABIT	O54814	ratius norv
44	492.5	27.1	359	1	IL6B_PABIT	P35407	ratius norv
45	491.5	27.0	352	1	CCR5_PAPHA	P56441	papio hamad

ALIGNMENTS

RESULT 1
ID CKRB_HUMAN STANDARD; PRT; 350 AA.
AC Q9NPB9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 11 (C-C CKR-11) (CC-CKR-11) (CCR-11)
DE (Chemokine receptor-like 1) (CRL1) (CCX CKR).
GN CCR1L OR CCR1L OR CCBP2 OR VSHK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20200450; PubMed=10734104;
RA Schweickart V.L., Epp A., Raport C.J., Gray P.W.;
RT "CCR11 is a functional receptor for the monocyte chemoattractant
protein family of chemokines.";
RL J. Biol. Chem. 275:9550-9556(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20171478; PubMed=10706668;
RA Goshing J., Dairagh D.J., Wang Y., Hanley M., Talbot D., Miao Z.,
Schall T.J.;
RT "Identification of a novel chemokine receptor that binds dendritic
cell- and T cell-activating chemokines including ELC, SLC, and TECK.";
RL J. Immunol. 164:2851-2856(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231748; PubMed=10767544;
RA Khoja H., Wang G., Ng C.-T.L., Tucker J., Brown T., Shyamala V.;
RT "Cloning of CCR11, an orphan seven transmembrane receptor related to
chemokine receptors, expressed abundantly in heart.";
RL Gene 246:229-238(2000).
RN [4]
RP SEQUENCE FROM N.A.
RX Koptez S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Receptor for SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4,
SCYA19/MIP3B/ELC, SCYA21/SLC and SCYA25/TECK.
CC -! SUBCELLULAR LOCATION: Integral membrane protein.
CC -! TISSUE SPECIFICITY: Predominantly expressed in heart. Lower
expression in lung, pancreas, spleen, small intestine and fetal
tissues.
CC -! SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Best Local Similarity 38.7%; Pred. No. 6,6e-34;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MLEGNOSRDYYEENEMNGTADYQYELICIKEDREFAKFLEPVLTIVFVIGLANS 60
Db 21 VLCCQDEVDDIGNT---TVDYTLFBSLCKSKVRFKMFLLIMSIICFGLGNG 77

QY 61 MYVAIYAYKKORTKTDVYIINLAVADLLFTLPFAVNAVHGVNGKINCKITSLY 120
Db 78 LVLTLYIYFKRLKMTDLYLNLAVADILFTLTFFMAVSAKSVFQVHCKLFLAYK 137

QY 121 LNFVSGMGLACISIDRYAVATKVP---OSGVKPCMIIFCYMAALISIPOLVFY 176
Db 138 MSFSGMMLLICISIDRYAVIQVSAHHRARVLLISTSCVGMITATVLSIDELYS 197

QY 177 TVNDNA---RCIPFPRYIGTSKAKLIQMLEICIGFVPEPLNGVCYFTARTLMKP 231
Db 198 DIQSSSEQAMCSSLITEH---VEAFITIQVQWYIGFVPEPLNMFCLVIRTLQAR 254

QY 232 NIKISRPILVLTIVFVITQLPNIVKFCRAIDIIYSLISCMNSKRMIDAIQVTE 291
Db 255 NFERNAIKVITAVVAVFVIFQLPNGVLAQTVANFNITSTCELSKQNLAIADVT 314

QY 292 ALFHSCLNPLLYFMGASFKNYMKVAKKYG-----SW-----RROSQVEPFPD 337
Db 315 ACVRCGVNPFVAFIVGKFRNDLFKFLKDLGCLSGQLRWMSCHIRRSMSVE---- 369

QY 338 SEGPTFTSTFS 349
Db 370 ---AETTTFS 377

RESULT 4
CKR7_MOUSE STANDARD; PRT; 378 AA.

AC P47774;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 7 precursor (C-C CKR-7) (CCR-7)
DE (MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1)
DE (EBI1)
GN CCR7 OR CMKBR7 OR EBI1 OR EBIH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CE7BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=9514835; PubMed=7851893;
RA Schwickert V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EBI1, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2";
RL Genomics 23:643-650 (1994).
CC -|- FUNCTION: Receptor for the MIP-3-beta chemokine. Probable mediator
CC of EBV effects on B lymphocytes or of normal lymphocyte functions.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC or send an email to license@isb-sib.ch).
CC EMBL; L31580; AAA74232.1; -
DR PIR; A55735; A55735.
DR MGD; MGI:103011; Ccr7.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IMP.

DR GO; GO:0006935; P:chemotaxis; IMP.
DR GO; GO:0006955; P:immune response; IMP.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECPT_P1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_P2_1; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 378
FT DOMAIN 25 59
FT TRANSSEM 60 86
FT DOMAIN 87 95
FT TRANSSEM 96 115
FT DOMAIN 117 130
FT TRANSSEM 131 152
FT DOMAIN 153 170
FT TRANSSEM 171 191
FT DOMAIN 192 219
FT TRANSSEM 220 247
FT DOMAIN 248 263
FT TRANSSEM 264 289
FT DOMAIN 290 313
FT TRANSSEM 314 331
FT DOMAIN 332 378
FT CARBOHYD 36 36
FT DISULFID 129 210
SQ SEQUENCE 378 AA; 42941 MW; ACB1A422CF54AAB54 CRC64;

Query Match 35.7%; Score 650; DB 1; Length 378;
Best Local Similarity 38.3%; Pred. No. 2,4e-33;
Matches 140; Conservative 67; Mismatches 125; Indels 34; Gaps 8;

QY 5 QNOSTDYVEENEMNGTADYQYELICIKEDREFAKFLEPVLTIVFVIGLANSWVA 64
Db 25 QDEVTDYIGENT---TVDYTLFBSLCKSKVRFKMFLLIMSIICFGLGNGVIL 81

QY 65 IYAYKKORTKTDVYIINLAVADLLFTLPFAVNAVHGVNGKINCKITSLYTLNFV 124
Db 82 TYIFFKLTKMTDLYLNLAVADILFTLTFFMAVSAKSVFQVHCKLFLAYK 141

QY 125 SGMQFLACISIDRYAVATKVP---OSGVKPCMIIFCYMAALISIPOLVFY 177
Db 142 SGMMLLICISIDRYAVIQVSAHHRARVLLISTSCVGMITATVLSIDELYS 198

QY 178 VNDNA---RCIPFPRYIGTSKAKLIQMLEICIGFVPEPLNGVCYFTARTLMKP 230
Db 199 LQKNSGEDTLRC---SLVSAQVEALITIQVQWYIGFVPEPLNMFCLVIRTLQAR 253

QY 231 NIKISRPILVLTIVFVITQLPNIVKFCRAIDIIYSLISCMNSKRMIDAIQVTE 290
Db 254 NFERNAIKVITAVVAVFVIFQLPNGVLAQTVANFNITSTCELSKQNLAIADVT 313

QY 291 IALFHSCLNPLLYFMGASFKNYMKVAKKYSWRFOR-----OSVEEFPDSEGPT 343
Db 314 LASVRCGVNPFVAFIVGKFRSDFKFLKDLGCLSGRLRWMSCHIRRNASVSM--AE 371

QY 344 PTSTFS 349
Db 372 TTTTFS 377

RESULT 5
CKR9_MOUSE STANDARD; PRT; 369 AA.

AC Q9WUT7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 9 (C-C CKR-9) (CCR-9)
DE (Chemokine C-C receptor 10).
GN CCR9 OR CMKBR10.
OS Mus musculus (Mouse).


```

CC EMBL: U45982; AAA93319.1; -.
DR EMBL: AY242127; AAO92294.1; -.
DR Genem: HGNC:1510; CCR6.
DR MIM: 604738; -.
DR GO: GO:0005887; C: integral to plasma membrane; TAS.
DR GO: GO:0004950; F: chemokine receptor activity; TAS.
DR GO: GO:0006968; P: cellular defense response; TAS.
DR GO: GO:0006935; P: chemotaxis; TAS.
DR GO: GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
DR GO: GO:0007186; P: G-protein coupled receptor protein signaling; .; TAS.
DR InterPro: IPR004069; CC: 9_receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO1531; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 37
FT TRANSMEM 38 64
FT DOMAIN 65 73
FT TRANSMEM 74 94
FT TRANSMEM 95 108
FT TRANSMEM 109 130
FT TRANSMEM 131 148
FT TRANSMEM 149 169
FT DOMAIN 170 198
FT TRANSMEM 199 226
FT TRANSMEM 227 242
FT TRANSMEM 243 268
FT TRANSMEM 269 292
FT TRANSMEM 293 310
FT TRANSMEM 311 357
FT CARBOHYD 20 20
FT DISULFID 107 186
SQ SEQUENCE 357 AA; 40713 MW; 96982E0B922FEB31 CRC64;

Query Match 35.0%; Score 637; DB 1; Length 357;
Best Local Similarity 36.5%; Pred. No. 1.4e-32;
Matches 119; Conservative 74; Mismatches 115; Indels 18; Gaps 4;

QY 10 DYYEE-NENNGTYDSQYELI-CKEDVREFAKFLPFLTLIVVIGLANSMTVAIYAY 68
DB 4 DYSESSTSSMEDVYVNFPTDFCEKQNVROFASHFLPYLVIVIGALNSILIVVY 63
QY 69 YKQRTKTDYIINLAVADILLFLTPPNAVNAVHGWLGKIMCKITSLYTLNPFSGWQ 128
DB 64 CTREKMTDMFLNLIAADLLFLVTLPEFAIAADQMKQTFENCKVNSMYKNTFSCVL 123
QY 129 FLACISIDRYVAATKVPSSQSGVKPCW-----IICFCVMAAILSLIPQVRYTVN 179
DB 124 LINCISIDRYIAIAQ-----AMRAHWREKRLYSKMGVCTIVVLAALCIPILYSQIK 178
QY 180 DN--ARCPITFPYLYSTSKALIQMLEICIGVAVPFLNGVCFYFTARTKIMPEIKS 236
DB 179 EESGIAICIMVYPSDESTKLKSAVLTILKVLGFELPFWAACCYTIIITHLQAKSSKH 238
QY 237 RPLKVLTLVIVVLTQLPYNIYKFCRAIDITSLTSCMSKRMIDIAQVESIALFHS 296
DB 239 KALNVTLTLVIVVLSQFPNCLILVOTIDAYAMFISNCASVINIDICGYVOTIAFHS 298
QY 297 CLNPIIVVFGASFKNVKVAKKYG 322
DB 299 CLNPIIVVFGERFRDLVTKNLIG 324

```

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DT 26-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 6 (C-C CR6) (CC-CR6) (Kv411).
GN CCR6 OR CCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yanagihara S., Komura E., Yamaguchi Y.,
RA Valona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
RA Albar J.P., Ardavin C., Marquez G.,
RT "Molecular cloning, functional characterization and mRNA expression
RT analysis of the murine chemokine receptor CCR6 and its specific ligand
RT MIP-3alpha".
RL FEBS Lett. 440:188-194 (1998).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-3-
CC alpha/LARC and subsequently transduces a signal by increasing the
CC intracellular calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL: AB009369; BA23776.1; -.
DR EMBL: AJ222714; CA10956.1; -.
DR MGD: MGI:133797; Ccr6.
DR GO: GO:0005515; F: protein binding; IPI.
DR InterPro: IPR004067; CC 6_receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO1529; GPCRHHODPSN.
DR PROSITE: PS00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 39
FT TRANSMEM 40 66
FT TRANSMEM 67 75
FT TRANSMEM 76 96
FT TRANSMEM 97 111
FT TRANSMEM 112 133
FT TRANSMEM 134 151
FT TRANSMEM 152 172
FT TRANSMEM 173 203
FT TRANSMEM 204 230
FT TRANSMEM 231 246
FT TRANSMEM 247 271
FT TRANSMEM 272 295
FT TRANSMEM 296 313
FT TRANSMEM 314 367
FT DISULFID 110 189
FT CARBOHYD 2 2
FT CARBOHYD 35 35
SQ SEQUENCE 367 AA; 42102 MW; 6A309AF83B117E CRC64;

Query Match 33.3%; Score 605; DB 1; Length 367;
Best Local Similarity 37.9%; Pred. No. 1.3e-30;
Matches 129; Conservative 60; Mismatches 125; Indels 26; Gaps 8;

QY 8 STDYIYENNGTYDSQYELI-CKEDVREFAKFLPFLTLIVVIGLANSMTVAIYAY 61

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Db 3 STEBYFETDD----YDNTETYSIPDPBPGSBERVFTKVPVPIANSLICGGLGNIM 58
 QY 62 VVAIAYKKKORTKTDVYIINLAVADILLFTLPEFNAV-NAVHGWLGKIMCKITSALYT 120
 Db 59 VVMVFAYKKARSMWTDVYLLNMATDILLFVLTLPFNAVTHATWVPSDLCKLMKGTVA 118
 QY 121 LNFPSGQGFACISIDRYVAVTKVPSQSGVGCW-----IICCVMAAILISIPOLVF 175
 Db 119 VNRPGCLLALCISMDRYIAIVQATKSPFRSRSLTHSKYICAAVMFISITISSPFIPIFN 178
 QY 176 --YTVNDNARCIPFPYLGTS---KCALIOMLEICIGFVPELIMGVCYFITARTLTK 229
 Db 179 KKYELQORDVC---EPFRYSVSEPIITWKLGMGLHLPFGFTLLFNVCYLPFIITVQ 235
 QY 230 MPNKRIRPKVLLTVIVIVFVQLEPNYIKFCRAIDITISLTSCMSGRMDIAQVTE 289
 Db 236 AONSKRRHRAKRVAVLAVLFLACIPHNWVLLVTAVA-TSKVRSCTEKVLAATRVNAE 294
 QY 290 SIALFHSCLNPILTVFMGASFKNYVMKAKKYGSRORQ 329
 Db 295 VLAFLHCCLPVLVYAFIGQKFRNVEFKIMEDVCMRRKKN 334

RESULT 8
 ID CKR6 HUMAN STANDARD; PRT; 374 AA.
 AC PS1684; P78553; Q92846;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 6 (C-C CKR-6) (CCR-6) (LARC receptor) (GPR-CY4) (GPRCY4) (Chemokine receptor-like 3) (CCR-L3) (DRY6).
 GN CKR6 OR CKMR6 OR STRL22 OR GPR29 OR CKRL3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND FUNCTION.
 RX MEDLINE=97313465; PubMed=9169459;
 RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K., Nomiyama H., Yoshie O.,
 RT "Identification of CKR6, the specific receptor for a novel lymphocyte-directed CC chemokine LARC.";
 RL J. Biol. Chem. 272:14893-14898 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lautens L.L., Modi W., Bonner T.I.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97040707; PubMed=886020;
 RA Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
 RT "Molecular cloning and RNA expression of two new human chemokine receptor-like genes.";
 RL Biochem. Biophys. Res. Commun. 227:846-853 (1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA McCoy R., Perlmutter D.H.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224503; PubMed=9070937;
 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled receptor related to chemokine receptors and located on chromosome 6q27.";
 RL Genomics 40:175-180 (1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Warren C.N., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction

RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22935763; PubMed=14574404;
 RA Mutsaers A.J., Palmer S.A., Sims S.K., Edwards C.A., Ahurst J.L., Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E., Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R., Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S., Babage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J., Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P., Blakey S., Bray-Tallen S., Brook J., Brown A.J., Brown J.Y., Burford D.C., Buttill W., Burton J., Carder C., Carter N.P., Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V., Collier K.E., Collins J.E., Coleman L.K., Corby N.R., Coville G.J., Culley K.M., Dhall P., Davies J., Dunn M., Earthrowl M.E., Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A., Frankland J., French L., Garner P., Garnett J., Ghori M.J., Gilby L.M., Gillson C.J., Githero R.J., Graham D.V., Grant M., Grigble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S., Hammond S., Harley U.L., Hart E.A., Heath P.D., Heathcote R., Holmes S.V., Howden P.V., Howe K.L., Howell G.R., Huckle E., Humphrey S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A., Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C., Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M., Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M., Maeslen G.L., Matthews L., McCann C.T., McLaren S.J., McMay K., McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T., Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R., Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W., Porter K.M., Ramsey Y., Randy S.A., Rice C.M., Ross M.T., Seale S.M., Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L., Squires S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J., Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B., Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L., Whitaker H., Wild A., Willey D.V., Wilmer T.E., Wood J.M., Wray P.W., Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A., Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;
 RL "The DNA sequence and analysis of human chromosome 6.";
 RN Nature 425:805-811 (2003).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Cantinai P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E., Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16889-16903 (2002).
 CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-3-alpha/LARC and subsequently transduces a signal by increasing the intracellular calcium ions level.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- TISSUE SPECIFICITY: Spleen, lymph nodes, appendix, and fetal liver. Expressed in lymphocytes, T cells and B cells but not in natural killer cells, monocytes or granulocytes.
 CC -I- INDUCTION: By interleukin-2.
 CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

FT TRANSMEM 144 164 4 (POTENTIAL).
 FT DOMAIN 165 187 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 188 215 5 (POTENTIAL).
 FT TRANSMEM 216 231 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 232 259 6 (POTENTIAL).
 FT TRANSMEM 260 275 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 276 293 7 (POTENTIAL).
 FT TRANSMEM 294 342 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 102 180 BY SIMILARITY.
 FT CARBOHYD 16 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT SEQUENCE 342 AA; 39226 MW; 6CBE389C6E5919E CRC64;

Query Match 31.9%; Score 581; DB 1; Length 342;
 Best Local Similarity 34.2%; Pred. No. 3.7e-29;
 Matches 121; Conservative 71; Mismatches 130; Indels 32; Gaps 8;

QY 12 YEENENMGTYDYSQYELICKEDEYREPAKVPFLVETIVFVIGLAGNSVVAIYAYKK 71
 DB 6 HYEDNGFNSFNDSSQEE---HODELQFSKVFPCMYLVVCGVGNSTLVVISIFYHK 61
 QY 72 QRTKDVYILMLAVALDILLFTLPFWANAVHGVGLKIMCKITSAITYTNFVSGMFLA 131
 DB 62 LOSLTDVFLVPLADLVFVCTLPFWAYAGIHEMIFGVWCKTLLGYITINFTSMILT 121
 QY 132 CISIDRYVAATKVPB--QSGVGKPCW--ITFCYMAAILLSIPQVFTV--NDNARCI 185
 DB 122 CITVDRIIVVAKATKAYNOQAKMTGWKVICLLIWIISLVSIPQIYGNVFNLDKIC- 180
 QY 186 PIFPRYLGTSKALIQMLEICIGFVFPFLNGCYFITTARTLMKMPNIKSRPLKVLTV 245
 DB 181 ---GYHDEESTVLTATQMTLGFPLAMIVCYSVIKTLHAGGFQKRSIKITFLV 236
 QY 246 VIVEFVITQLPYNIYVFCRAIDIIYSLTSCNMSKMDIAIQVTSIALFHSCLNPILYVF 305
 DB 237 MAVFLITQTPNIVKILRSTHMEYAMTSFHYT-----IIVTEALAYLRACINPVLYAF 290
 QY 306 MGASFKNYVKKVAKKYG-----SMRQROSVVEFPDSEPTPTSTFST 350
 DB 291 VSLKFRKFMKLVKDIGCLPYLGVSHOKSSEDSNKK--TFSASHNVATSMFQL 342

RESULT 10

CCRE6_MACNE STANDARD; PRT; 343 AA.
 AC Q9X143;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-X-C chemokine receptor type 6 (CXCR-6) (G protein-coupled receptor bonzo) (G protein-coupled receptor STRL33).
 GN CXCR6 OR BONZO OR STRL33.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
 NCBI_Taxid=9544;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=21354176; PubMed=11461684;
 RA Margulies B.J., Haer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine receptors";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
 CC - FUNCTION: Receptor for the C-X-C chemokine CXCL16. Used as a coreceptor by HIV and by strains of HIV-2 and m-tropic HIV-1.
 CC - SUBCELLULAR LOCATION: Integral membrane protein.
 CC - SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC EMBL; AF124380; AAD31419.1; -
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PRO0237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 FT G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 33
 FT TRANSMEM 34 60
 FT TRANSMEM 61 69
 FT TRANSMEM 70 90
 FT TRANSMEM 91 104
 FT TRANSMEM 105 126
 FT TRANSMEM 127 144
 FT TRANSMEM 145 165
 FT TRANSMEM 166 188
 FT TRANSMEM 189 216
 FT TRANSMEM 217 232
 FT TRANSMEM 233 260
 FT TRANSMEM 261 276
 FT TRANSMEM 277 294
 FT TRANSMEM 295 343
 FT CARBOHYD 17 17
 FT DISULFID 103 181
 SQ SEQUENCE 343 AA; 39423 MW; 48DB2544949EB83F CRC64;

Query Match 31.4%; Score 571; DB 1; Length 343;
 Best Local Similarity 33.4%; Pred. No. 1.5e-28;
 Matches 119; Conservative 73; Mismatches 132; Indels 32; Gaps 8;

QY 10 DYEEENMGTYDYSQYELICKEDEYREPAKVPFLVETIVFVIGLAGNSVVAIYAY 69
 DB 5 DYEDNGFNSFNDSSQEE---HODELQFSKVFPCMYLVVCGVGNSTLVVISIFY 60
 QY 70 KQRTKDVYILMLAVALDILLFTLPFWANAVHGVGLKIMCKITSAITYTNFVSGMFL 129
 DB 61 HKQSLTDVFLVPLADLVFVCTLPFWAYAGIHEMIFGVWCKTLLGYITINFTSMILT 120
 QY 130 LACISIDRYVAATKVPB--QSGVGKPCW--ITFCYMAAILLSIPQVFTV--NDNAR 183
 DB 121 LTCITVDRIIVVAKATKAYNOQAKMTGWKVICLLIWIISLVSIPQIYGNVFNLDKIL 180
 QY 184 CIPFPRYLGTSKALIQMLEICIGFVFPFLNGCYFITTARTLMKMPNIKSRPLKVL 243
 DB 181 C---GYHDEESTVLTATQMTLGFPLAMIVCYSVIKTLHAGGFQKRSIKITFL 235
 QY 244 TVIVFVITQLPYNIYVFCRAIDIIYSLTSCNMSKMDIAIQVTSIALFHSCLNPILY 303
 DB 236 LVAWVFLITQTPNIVKILRSTHMEYAMTSFHYT-----IIVTEALAYLRACINPVLY 289
 QY 304 VFMGASFKNYVKKVAKKYG-----SMRQROSVVEFPDSEPTPTSTFST 350
 DB 290 AFVSLKFRKFMKLVKDIGCLPYLGVSHOKSSEDSNKK--TFSASHNVATSMFQL 343

RESULT 11

CCRE6_MACNE STANDARD; PRT; 342 AA.
 AC O19024;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-X-C chemokine receptor type 6 (CXCR-6) (G protein-coupled receptor bonzo).
 GN CXCR6 OR BONZO.
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
 NCBI_Taxid=9545;

```

RN  [1]
SEQUENCE FROM N.A.
RX MEDLINE=97373956; PubMed=9230441;
RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
RT "Expression cloning of new receptors used by simian and human
   immunodeficiency viruses."
RL Nature 388:296-300(1997).
CC -1- FUNCTION: Receptor for the C-X-C chemokine CXCL16. Used as a
   coreceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF007858; AAB64224.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32
FT TRANSSEM 33 59
FT DOMAIN 60 68
FT TRANSSEM 69 89
FT DOMAIN 90 103
FT TRANSSEM 104 125
FT DOMAIN 126 143
FT TRANSSEM 144 164
FT DOMAIN 165 187
FT TRANSSEM 188 215
FT TRANSSEM 216 231
FT TRANSSEM 232 259
FT TRANSSEM 260 275
FT TRANSSEM 276 293
FT DOMAIN 294 342
FT DISULFID 102 180
FT CARBOHYD 16
SQ SEQUENCE 342 AA; 39297 MW; 55F9F68CB62D2DF5 CRC64;

Query Match 31.1%; Score 569; DB 1; Length 342;
Best Local Similarity 33.6%; Pred. No. 28-28;
Matches 119; Conservative 72; Mismatches 131; Indels 32; Gaps 8;

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RESULT 12
CGR6_MACFA STANDARD; PRT; 343 AA.
AC 09SDS6;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled
   receptor homoz) (G protein-coupled receptor STRL33).
DE CXCR6 OR BOMZO OR STRL33
CN Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21134756; PubMed=11242524;
RA Wade-Evans A.M., Russell J., Jenkins A., Javan C.;
RT "Cloning and sequencing of cynomolgus macaque ccr3, gpri5, and strl33:
   potential coreceptors for HIV type 1, HIV type 2, and SIV."
RL AIDS Res. Hum. Retroviruses 17:371-375(2001).
CC -1- FUNCTION: Receptor for the C-X-C chemokine CXCL16. Used as a
   coreceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF291671; AAK25742.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 33
FT TRANSSEM 34 60
FT DOMAIN 61 69
FT TRANSSEM 70 90
FT TRANSSEM 91 104
FT DOMAIN 105 126
FT TRANSSEM 127 144
FT DOMAIN 145 165
FT TRANSSEM 166 188
FT TRANSSEM 189 215
FT TRANSSEM 217 232
FT DOMAIN 233 260
FT TRANSSEM 261 276
FT DOMAIN 277 294
FT TRANSSEM 295 343
FT CARBOHYD 17
FT DISULFID 103 181
SQ SEQUENCE 343 AA; 39472 MW; 0961328F948E7784 CRC64;

Query Match 31.1%; Score 566; DB 1; Length 343;
Best Local Similarity 33.1%; Pred. No. 38-28;
Matches 118; Conservative 73; Mismatches 133; Indels 32; Gaps 8;

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Db 61 HKQSLTVLVLNPLADLVFCTLPFWTYAGIHENIFQWCKLLGVYITINFTSMLI 120
 QY 130 LACISIDRYAVATKVPSS--QSGVGRKPC--IICFCVMAAILSLPOLVFYTV--NDNAR 183
 Db 121 LNCITADRIIVVAKTKATKANOQAKMTKGVCLILINVSILVSLPQIYGVNFMIDKLI 180
 QY 184 CIPIFPRYIGTSMKALICMLEICIGFVPELLMGVCYFITAFTLMKPNIKISPLKXVL 243
 Db 181 C-----GYHDEISITVLAOTMGLFPLMLAMICVSYIITLLHAGGFQGRSLKTIIF 235
 QY 244 TVIVIVITVQLPYNIVKFCRAIDIIYSILTSQNMKRMIDAIQVETALFHSCLNPIY 303
 Db 236 LMAVAVLLIQTFFNLVKTIRSTRMEYANTSPHYT-----ITVEALAYLRACINPVLY 289
 QY 304 VFMGASFKYVNVKVAKKYG-----SWRROROSVEEPFDSGPTPEPTSPSI 350
 Db 290 AFVSLTKFRKNFMVLVDICGLPYLGVSQWKSSEDNSK--TTSASHNVEATSMFQL 343

RESULT 13

CCR6_HUMAN STANDARD; PRT; 342 AA.

AC 000574; 000575; 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DE 15-MAR-2004 (Rel. 43, Last annotation update)

DE C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled

receptor bonzo) (G protein-coupled receptor STRL33).

OS CXCR6 OR BONZO OR STRL33 OR TYMSTR.

GN Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=97373958; PubMed=9230441;

RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;

RT "Expression cloning of new receptors used by simian and human

immunodeficiency viruses.";

RL Nature 388:296-300(1997).

RN [2]

RP SEQUENCE FROM N.A., AND VARIANT ALA-25.

RA MEDLINE=97311099; PubMed=9166430;

RA Liao F., Alkhatib G., Paden K.W.C., Sharma G., Berger E.A.,

RA Farber J.M.;

RT "STRL33, A novel chemokine receptor-like protein, functions as a

fusion cofactor for both macrophage-tropic and T cell line-tropic

HIV-1.";

RL J. Exp. Med. 185:2015-2023(1997).

RN [3]

RP SEQUENCE FROM N.A.

RA TISSUE=Blood;

RA MEDLINE=97431687; PubMed=9285716;

RA Loetscher M., Amara A., Oberlin B., Brase N., Legler D.F.,

RA Baggiolini M., Arenzana-Seisdedos F., Moser B., Virelizier J.L.,

RT "TYMSTR, a putative chemokine receptor selectively expressed in

activated T cells, exhibits HIV-1 coreceptor function.";

RL Curr. Biol. 7:652-660(1997).

RN [4]

RP SEQUENCE FROM N.A.

RA Kopalitz S.A., Atkinson R.S., Sharma S.V.;

RT "cDNA clones of human proteins involved in signal transduction

sequenced by the Gutthrie cDNA resource center (www.cdna.org).";

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RA TISSUE=Pancreas;

RA MEDLINE=22388257; PubMed=12477932;

RA Strassberg R.W., Felingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buecaw K.H., Scheffer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stipitonen M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Cantucci P., Prange C.J.,
 RA Rana S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.U., McKernan K.J., Melex J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smellus D.E.,
 RA Schnerch A., Schein J.E., Jones S.U.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Receptor for the C-X-C chemokine CXCL16. Used as a
 CC coreceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in lymphoid tissues and activated T
 CC cells.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF007545; AAB64221.1; -;
 DR EMBL; U73529; AAB61456.1; -;
 DR EMBL; U73531; AAB61457.1; -;
 DR EMBL; Y13248; CAA73698.1; -;
 DR EMBL; AY322543; AAB84356.1; -;
 DR EMBL; BC033584; AAB84356.1; -;
 DR Genew; HGNC:16647; CXCR6.
 DR MIM; 605163; -;
 DR GO; GO:0003887; C: integral to plasma membrane; TAS.
 DR GO; GO:0015026; F: coreceptor activity; TAS.
 DR GO; GO:0004930; F: G-protein coupled receptor activity; TAS.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signaling; TAS.
 DR GO; GO:0008166; P: viral replication; TAS.
 DR InterPro; IPR00276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm1.1;
 DR PRINTS; PR00237; GPCR_RHOPOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
 FT DOMAIN 1 32
 FT TRANSSEM 33 59
 FT DOMAIN 60 68
 FT TRANSSEM 69 89
 FT DOMAIN 90 103
 FT TRANSSEM 104 125
 FT DOMAIN 126 143
 FT TRANSSEM 144 164
 FT DOMAIN 165 187
 FT TRANSSEM 188 215
 FT DOMAIN 216 231
 FT TRANSSEM 232 259
 FT DOMAIN 260 275
 FT TRANSSEM 276 293
 FT DOMAIN 294 342
 FT DISUFID 102 180
 FT CARBOHYD 16 16
 FT VARIANT 25 25
 SQ SEQUENCE 342 AA; 39280 MW; 9FBC02556D1082E CRC64;
 Query Match 30.8%; Score 560; DB 1; Length 342;
 Best Local Similarity 33.1%; Pred. No. 7, 1e-28;

Matches 117; Conservative 75; Mismatches 130; Indels 32; Gaps 8;

QY 12 YEEENKNGTADYSQYELICIKEDVEEFAKFLPVFLTFVIFGLAGNSMVAIYAYKK 71
 DB 6 YHEDYGFNSFSDSSE-----HODPLQSKVFLPCMIVLVFVGLVGNLSLVISIFYK 61

QY 72 QRTKTDVILINAVADLLFLTFPMAVAVHGVLTGIMCKITSAIYTLNFSGMQFLA 131
 DB 62 LQSLTDVFLVNLPLADLVFVCTLPFWAVAGIHEWFGVWCKSLIGIYITINFTSMILT 121

QY 132 CISIDRYAVATKVPB--QSGVGKPCW--IICFCVMAAILISIPOLVFTV--NDNARCI 185
 DB 122 CITVDFRIVVAVATKAVYNOQAKRMVGTSLIIVISLISLQIITIGVFNIDKILC- 180

QY 186 PIFPRYLGTSKMLIQMLEICIGFVFPFLIMGVCYFITARLTKMKNIKISRLKVLTV 245
 DB 181 ----GYHDEAISTVLATQMTLGFPLPLTMIVCYSVIIKTLHAGGFQKRSIKIIFLV 236

QY 246 VIVFIVTQLPYNIIVKRCALDIYSLITSCNMSKMDIALIOVTSIALFHSCLNPLIYF 305
 DB 237 MAVFLLTQMPFNLMKIRSTHWEYAMTSFHT-----IMVTERAIYLRACLNPLIYAF 290

QY 306 MGASFKNVYWKVAKKYG-----SWRQROSVVEEPPDSBGPTEPTSTFSI 350
 DB 291 VSLKFRKNFWKLVDIGCLPYLGVSHPKSSSEDSNK--TFSSHVNEATSMFOL 342

RESULT 14

CCR6_PANTR STANDARD; PRT; 342 AA.

AC Q9TV16;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled receptor bonzo) (G protein-coupled receptor STRL33).
 GN CXCR6 OR BONZO OR STRL33.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
 NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=943349; PubMed=10505680;
 RA Brussel A., Preter J.-L., Girard M., Butor C.;
 RT "Sequences and predicted structures of chimpanzee STRL33 (Bonzo) and gp135 (BOB).";
 RL AIDS Res. Hum. Retroviruses 15:1315-1319(1999).
 CC -1- FUNCTION: Receptor for the C-X-C chemokine CXCL16. Used as a coreceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC EMBL: AF084229; AAD52041.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; Tm1.1;
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1;
 DR PROSITE: PS02622; G_PROTEIN_RECPT_F1_2; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 32
 FT TRANSMEM 33 59
 FT TRANSMEM 60 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 103
 FT DOMAIN EXTRACELLULAR (POTENTIAL).

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 FT DOMAIN 126 143
 FT TRANSMEM 144 164
 FT DOMAIN 165 187
 FT TRANSMEM 188 215
 FT DOMAIN 216 231
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 FT DOMAIN 260 275
 FT TRANSMEM 276 293
 FT DOMAIN 294 342
 FT DISULFID 102 180
 FT CARBOHYD 16 16
 SQ SEQUENCE 342 AA; 39273 MW; 5585803797806B2A CRC64;

Query Match 30.7%; Score 559; DB 1; Length 342;
 Best Local Similarity 33.1%; Pred. No. 8.2e-28;
 Matches 117; Conservative 74; Mismatches 131; Indels 32; Gaps 8;

QY 12 YEEENKNGTADYSQYELICIKEDVEEFAKFLPVFLTFVIFGLAGNSMVAIYAYKK 71
 DB 6 YHEDYGFNSFSDSSE-----HODPLQSKVFLPCMIVLVFVGLVGNLSLVISIFYK 61

QY 72 QRTKTDVILINAVADLLFLTFPMAVAVHGVLTGIMCKITSAIYTLNFSGMQFLA 131
 DB 62 LQSLTDVFLVNLPLADLVFVCTLPFWAVAGIHEWFGVWCKSLIGIYITINFTSMILT 121

QY 132 CISIDRYAVATKVPB--QSGVGKPCW--IICFCVMAAILISIPOLVFTV--NDNARCI 185
 DB 122 CITVDFRIVVAVATKAVYNOQAKRMVGTSLIIVISLISLQIITIGVFNIDKILC- 180

QY 186 PIFPRYLGTSKMLIQMLEICIGFVFPFLIMGVCYFITARLTKMKNIKISRLKVLTV 245
 DB 181 ----GYHDEAISTVLATQMTLGFPLPLTMIVCYSVIIKTLHAGGFQKRSIKIIFLV 236

QY 246 VIVFIVTQLPYNIIVKRCALDIYSLITSCNMSKMDIALIOVTSIALFHSCLNPLIYF 305
 DB 237 MAVFLLTQMPFNLMKIRSTHWEYAMTSFHT-----IMVTERAIYLRACLNPLIYAF 290

QY 306 MGASFKNVYWKVAKKYG-----SWRQROSVVEEPPDSBGPTEPTSTFSI 350
 DB 291 VSLKFRKNFWKLVDIGCLPYLGVSHPKSSSEDSNK--TFSSHVNEATSMFOL 342

RESULT 15

CCR4_HUMAN STANDARD; PRT; 360 AA.

AC P51679; Q9ULY6; Q9ULY7;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 4 (C-C CR-4) (CCR-4) (CCR4) (KS-5).
 GN CCR4 OR CCR4.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISUE=Sp1en;
 RX MEDLINE=95370289; PubMed=7642634;
 RA Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogwerf A.D., Proudfoot A.E.I., Wells T.N.C.;
 RT "Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human basophilic cell line.";
 RL J. Biol. Chem. 270:19495-19500(1995).
 RN SEQUENCE FROM N.A. AND VARIANTS VAL-130 AND SER-178.
 RX MEDLINE=21040311; PubMed=11196669;
 RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H., Hirai K., Tokunaga K.;
 RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
 RL Genes Immun. 1:97-104(1999).

RN [3] SEQUENCE FROM N.A.
 RP Kopravz S.A., Aronstam R.S., Sharma S.V.;
 RA "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP FUNCTION.
 RX MEDLINE=97313486; PubMed=9169480;
 RA Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;
 RT "The T cell-directed CC chemokine TARC is a highly specific
 RL biological ligand for CC chemokine receptor 4.";
 RN J. Biol. Chem. 272:15036-15042(1997).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=98104168; PubMed=9430724;
 RA Imai T., Chantry D., Raport C.D., Wood C.L., Nishimura M., Godiska R.,
 RL Yoshie O., Gray P.W.;
 RT "Macrophage-derived chemokine is a functional ligand for the CC
 RN chemokine receptor 4.";
 RL J. Biol. Chem. 273:1764-1768(1998).
 RN [6]
 RP FUNCTION.
 RX MEDLINE=99394604; PubMed=1046728;
 RA Campbell J.J., Haraldsen G., Pan J., Rottman J., Qin S., Ponath P.,
 RL Andrew D.P., Marinko R., Ruffing N., Kassam N., Wu L., Butcher E.C.;
 RT "The chemokine receptor CCR4 in vascular recognition by cutaneous but
 RN not intestinal memory T cells.";
 RL Nature 400:776-780(1999).
 RN [7]
 RP FUNCTION, TISSUE SPECIFICITY, AND PHOSPHORYLATION.
 RX MEDLINE=20219238; PubMed=10754297;
 RA Ingberdingen M., Danaj B., Maghazachi A.A.;
 RT "Human NK cells express CC chemokine receptors 4 and 8 and respond to
 RN thymus and activation-regulated chemokine, macrophage-derived
 RL chemokine, and I-309.";
 RL J. Immunol. 164:4048-4054(2000).
 CC -1- FUNCTION: High affinity receptor for the C-C type chemokines
 CC TARC/SCYA17 and MDC/SCYA22. The activity of this receptor is
 CC mediated by G(i) proteins which activate a phosphatidylinositol-
 CC calcium second messenger system. Can function as a chemotactic
 CC homing receptor on circulating memory lymphocytes and as a
 CC coreceptor for some primary HIV-2 isolates. In the CNS, could
 CC mediate hippocampal-neuron survival.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Predominantly expressed in the thymus, in
 CC peripheral blood leukocytes, including T cells, mostly cd4+ cells,
 CC and basophils, and in platelets; at lower levels, in the spleen
 CC and in monocytes. Detected also in macrophages, IL-2-activated
 CC natural killer cells and skin-homing memory T cells, mostly the
 CC ones expressing the cutaneous lymphocyte antigen (CLA). Expressed
 CC in brain microvascular and coronary artery endothelial cells.
 CC -1- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
 CC PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY
 CC BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC EMBL; AB024255; BAA87332.1; -
 CC EMBL; AB024256; BAA87333.1; -
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 CC EMBL; AB024258; BAA87335.1; -
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 CC EMBL; AB024260; BAA87337.1; -
 CC EMBL; AB024261; BAA87338.1; -
 CC EMBL; AB024262; BAA87339

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OM protein - protein search, using sw model

Run on: April 13, 2004, 13:15:19 / Search time 45 Seconds
(without alignments)
2454.030 Million cell updates/sec

Title: US-09-721-341-2
Perfect score: 1819
Sequence: 1 MALENGQSDYVYEEENMG.....VRRFPDSEGPTEPTSTPSI 350

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

SPREMBL_25:
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1596	87.7	350	11 Q92413	Q92413 mus musculus
2	1594	87.6	350	11 Q8COM1	Q8COM1 mus musculus
3	1593	87.6	350	11 Q8Q2W9	Q8Q2W9 mus musculus
4	912	50.1	221	11 Q9ESX1	Q9ESX1 rattus norv
5	657	36.1	378	6 Q8HZR6	Q8HZR6 macaca mula
6	648	35.6	380	11 Q8CA52	Q8CA52 mus musculus
7	645.5	35.5	380	6 Q8G1S1	Q8G1S1 sus scrofa
8	643	35.3	389	4 Q9U0Q6	Q9U0Q6 homo sapien
9	643	35.3	369	11 Q8CH33	Q8CH33 rattus norv
10	611	33.6	367	11 Q9R1V0	Q9R1V0 mus musculus
11	586.5	32.2	368	6 Q84444	Q84444 oncorhynch
12	583	32.1	374	6 Q8HZR7	Q8HZR7 macaca mula
13	578	31.8	343	6 Q9N0Z0	Q9N0Z0 cercopithec
14	566.5	31.1	351	11 Q9E016	Q9E016 mus musculus
15	566	31.1	343	6 Q9BDS6	Q9BDS6 macaca fasc
16	561.5	30.9	351	11 Q9ERH5	Q9ERH5 mus musculus

17	560	30.8	342	4 Q9HC45	Q9HC45 homo sapien
18	559	30.7	342	6 Q9TV16	Q9TV16 pan troglod
19	554	29.9	358	13 Q9PUA0	Q9PUA0 acipenser r
20	535.5	29.4	355	6 Q8HZN7	Q8HZN7 gorilla gor
21	534.5	29.4	355	4 Q8IU21	Q8IU21 homo sapien
22	534.5	29.4	355	6 Q8HZN8	Q8HZN8 pan troglod
23	534.5	29.4	355	6 Q8HZN6	Q8HZN6 pongo pygma
24	531.5	29.2	360	6 Q8MJW8	Q8MJW8 canis famil
25	529	29.1	351	11 Q8VHP3	Q8VHP3 cavia porce
26	527	29.0	384	4 Q8CBU0	Q8CBU0 homo sapien
27	525.5	28.9	360	11 Q91ZH4	Q91ZH4 rattus norv
28	521.5	28.7	358	13 Q7XUJ7	Q7XUJ7 xenopus lae
29	520.5	28.6	358	13 Q9YGC3	Q9YGC3 xenopus lae
30	516.5	28.4	355	6 Q8HZN3	Q8HZN3 papio hamad
31	516	28.4	355	11 Q9JLY8	Q9JLY8 rattus norv
32	515	28.3	384	4 Q7Z711	Q7Z711 homo sapien
33	513	28.2	354	11 Q8CBU0	Q8CBU0 mus musculus
34	511	28.1	354	11 Q8BR50	Q8BR50 mus musculus
35	508	27.9	355	6 Q8HZN5	Q8HZN5 macaca mula
36	507.5	27.9	347	6 Q9MZN1	Q9MZN1 eulemur mac
37	507	27.9	357	13 Q42445	Q42445 oncorhynch
38	506.5	27.8	347	6 Q9MZN6	Q9MZN6 callimico g
39	506.5	27.8	347	6 Q9MZN7	Q9MZN7 ceropithec
40	505.5	27.8	355	6 Q8HZN4	Q8HZN4 petromyzon
41	505.5	27.8	374	13 Q80ZHI	Q80ZHI alouatta se
42	503.5	27.7	347	6 Q9MZN0	Q9MZN0 alouatta se
43	503.5	27.7	352	6 Q9TV44	Q9TV44 cercopithec
44	502.5	27.6	347	6 Q9MZP1	Q9MZP1 mandillus
45	502.5	27.6	347	6 Q9MZN5	Q9MZN5 pithecia pl

ALIGNMENTS

RESULT 1

Q92413 ID Q92413 PRELIMINARY: PRT: 350 AA.

AC 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Chemokine receptor CCR1.
CN CCR1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;

RX MEDLINE=20519697; PubMed=11063828;

RA Dorr M.E., Berman M.A., Tanabe S., Heesen M., Luo Y.;

RT "Astrocytes express functional chemokine receptors.";

RL J. Neuroimmunol. 111:109-121(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

EMBL: AF306532; AAK81712.1; -

EMBL: AK042430; BAC31258.1; -

MDL: MGI:2181676; CCR1.

GO: GO:0016021; C:Integral to membrane; IEA.

GO: GO:0016493; F:C-C chemokine receptor activity; IEA.

GO: GO:0004872; F:receptor activity; IEA.

GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO: GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.

InterPro: IPR005183; CC 11 receptor.

InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7em.1; 1.
 DR PRINTS: PRO1558; CHEMOKINER11.
 DR PRINTS: PRO0237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G_PROTEIN_REC_P1.1; 1.
 DR PROSITE: PS0262; G_PROTEIN_REC_P2.1; 1.
 DR RECEPTOR.
 KW SEQUENCE 350 AA; 39530 MW; C5F7D9DC949CECF CRC64;

Query Match 87.7%; Score 1596; DB 11; Length 350;
 Best Local Similarity 85.4%; Pred. No. 9.2e-11;
 Matches 299; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

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 DB 1 MLELQNSAEYEEENENNGTYDSQYEVICIKEDVREFAKFLPVLFTIVFTGLAGNS 60
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 DB 61 VVAATYAYKKORTDYIINLAVADLLFTLPFAVNAVHGMVLTGKIMCKTSLALT 120
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 DB 121 VNFVSGMQLACISIDRYAVATKVPDSQSGVKPCMIICCCVMAAILLSIPQVFTVND 180
 QY 121 VNFVSGMQLACISIDRYAVATKVPDSQSGVKPCMIICCCVMAAILLSIPQVFTVND 180
 DB 121 VNFVSGMQLACISIDRYAVATKVPDSQSGVKPCMIICCCVMAAILLSIPQVFTVND 180
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 DB 241 VLLTVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKMDIAIQVTSIALFSCINP 300
 QY 301 ILVFMGASFKNYVMKAKKYGSWRRQOSVSEPPFDEGTEPTSTFSI 350
 DB 301 ILVFMGASFKNYVMKAKKYGSWRRQOSVSEPPFDEGTEPTSTFSI 350

RESULT 2

08QCM1 PRELIMINARY; PRT; 350 AA.

AC 08QCM1.
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Chemokine receptor CCR11 homolog.
 GN CCR11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK030643; BAC27061.1; -
 DR MGD; MGI:2181676; Ccr11.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR005383; CC_11_receptor.
 DR InterPro; IPR00276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7em.1; 1.
 DR PRINTS; PRO1558; CHEMOKINER11.
 DR PRINTS; PRO0237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_REC_P1.1; 1.
 DR PROSITE; PS0262; G_PROTEIN_REC_P2.1; 1.
 SQ SEQUENCE 350 AA; 39562 MW; DAACD9D798E5A13 CRC64;

Query Match 87.6%; Score 1594; DB 11; Length 350;
 Best Local Similarity 85.4%; Pred. No. 1.4e-130;
 Matches 299; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

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 DB 1 MLELQNSAEYEEENENNGTYDSQYEVICIKEDVREFAKFLPVLFTIVFTGLAGNS 60
 QY 61 MVAATYAYKKORTDYIINLAVADLLFTLPFAVNAVHGMVLTGKIMCKTSLALT 120
 DB 61 VVAATYAYKKORTDYIINLAVADLLFTLPFAVNAVHGMVLTGKIMCKTSLALT 120
 QY 121 LNFVSGMQLACISIDRYAVATKVPDSQSGVKPCMIICFCVMAAILLSIPQVFTVND 180
 DB 121 VNFVSGMQLACISIDRYAVATKVPDSQSGVKPCMIICCCVMAAILLSIPQVFTVND 180
 QY 121 VNFVSGMQLACISIDRYAVATKVPDSQSGVKPCMIICCCVMAAILLSIPQVFTVND 180
 DB 121 VNFVSGMQLACISIDRYAVATKVPDSQSGVKPCMIICCCVMAAILLSIPQVFTVND 180
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 DB 181 NARCFIPFRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNIKISPLK 240
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 DB 241 VLLTVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKMDIAIQVTSIALFSCINP 300
 QY 301 ILVFMGASFKNYVMKAKKYGSWRRQOSVSEPPFDEGTEPTSTFSI 350
 DB 301 ILVFMGASFKNYVMKAKKYGSWRRQOSVSEPPFDEGTEPTSTFSI 350

RESULT 3

08QZM9 PRELIMINARY; PRT; 350 AA.

AC 08QZM9.
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Chemokine receptor CCX CKR.
 GN CCR11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RA Tomason J.R., Nibbs R.J.;
 RT "Characterization of mouse CCX CKR, a receptor for the lymphocyte-
 RT attracting chemokines TRCK (CCL25), SLC (CCL21) and MIP-3beta (CCL19):
 RT comparison to human CCX CKR."
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY072796; AAL68400.1; -
 DR MGD; MGI:2181676; Ccr11.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR005383; CC_11_receptor.
 DR InterPro; IPR00276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7em.1; 1.
 DR PRINTS; PRO1558; CHEMOKINER11.
 DR PRINTS; PRO0237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_REC_P1.1; 1.
 DR PROSITE; PS0262; G_PROTEIN_REC_P2.1; 1.
 KW RECEPTOR.
 SQ SEQUENCE 350 AA; 39544 MW; D017CC29749CECD5 CRC64;

Query Match 87.6%; Score 1593; DB 11; Length 350;
 Best Local Similarity 85.1%; Pred. No. 1.7e-130;
 Matches 298; Conservative 27; Mismatches 25; Indels 0; Gaps 0;

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Db 1 MLELNQSAHEYYEENKNGTYDYSOYELICIKEDVEBAKFLPVLITVIVIGLAGNS 60
QY 61 MVAIYAYKQRTKTDYIINLAVADLLFLTPPMVAVNHGVLGKIMCKITSALYT 120
Db 61 VVAIYAYKQRTKTDYIINLAVADLLFLTPPMVAVNHGVLGKIMCKITSALYT 120
QY 121 LNFVSGMOPLACISIDRYAVATKVPDSQSGVKPCNICGVMAAILLSIPOLVYTVND 180
Db 121 VNFVSGMOPLACISIDRYAVATKVPDSQSGVKPCNICGVMAAILLSIPOLVYTVND 180
QY 181 NARCIPIPRVYLGTSKALIQMLEICIGFVPEFLMGVCYFITAATLMKMPNIXISPLK 240
Db 181 NARCIPIPRVYLGTSKALIQMLEICIGFVPEFLMGVCYFITAATLMKMPNIXISPLK 240
QY 241 VLLTVIVIVITQLPYINIVKFCRAIDIIYSLTSCNMSKRMIDIAQVETALPHSCINP 300
Db 241 VLLAVVAVIVITQLPYINIVKFCRAIDIIYSLTSCNMSKRMIDIAQVETALPHSCINP 300
QY 301 ILYVFMGASFKYVYVMAKKGYSWRQSQVSEFPDSEGPTEPTSTPSI 350
Db 301 ILYVFMGASFKYVYVMAKKGYSWRQSQVSEFPDSEGPTEPTSTPSI 350

RESULT 4
Q9ESK1 PRELIMINARY; PRT; 221 AA.
AC Q9ESK1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative G-protein coupled receptor GPCR14 (fragment).
GN GPCR14.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Harlan Sprague-Dawley;
RC Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;
RT "Identification and characterization of novel G-protein coupled
RT receptors expressed in regenerating peripheral nerve."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090348; AAC24470.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaling. .; IEA.
DR InterPro; IPR005382; CC_10_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO1557; CHEMOKINER10.
DR PROSITE; PRO0237; GPCR_HODOPSIN.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
KM Receptor.
FT NON_TER 1 1
FT NON_TER 221 221
SQ SEQUENCE 221 AA; 24342 MW; 5622DD6073738A6C CRC64;

Query Match 50.1%; Score 912; DB 11; Length 221;
Best Local Similarity 83.3%; Pred. No. 1.9e-71;
Matches 169; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 96 FMAVNAVHGVVJGKIMCKITSALYTINIVSGMOPLACISIDRYAVATKVPDSQSGVKPCW 155
Db 19 FMAVNAVHGVVJGKIMCKITSALYTINIVSGMOPLACISIDRYAVATKVPDSQSGVKPCW 78
QY 156 IIFCVMAAILLSIPOLVYTVNDNARCIPIPRVYLGTSKALIQMLEICIGFVPEFLI 215

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Db 79 ICCCVTAAILLSIPOLVYTVNENARCTPVPFHHGLTSKASIQMLEIFIGFVPEFLI 138
QY 216 MGVCYFITAATLMKMPNIXISPLKYLITVIVITQLPYINIVKFCRAIDIIYSLTSC 275
Db 139 MGVCYFITAATLMKMPNIXISPLKYLITVIVITQLPYINIVKFCRAIDIIYSLTSC 198
QY 276 NMSKRMIDIAQVETALPHSCL 298
Db 199 NMSKRMIDIAQVETALPHSCL 221

RESULT 5
Q8H2R6 PRELIMINARY; PRT; 378 AA.
AC Q8H2R6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CC chemokine receptor 7.
GN CCR7.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
RX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=24471764; PubMed=12406887;
RC Choi Y.K., Fallert B.A., Murhey-Corb M.A., Reinhart T.A.;
RT "Simian immunodeficiency virus dramatically alters expression of
RT homeostatic chemokines and dendritic cell markers during infection in
RT vivo."
RL Blood 101:1684-1691 (2003).
DR EMBL; AF508731; AAN47099.2; -.
KM Receptor.
SQ SEQUENCE 378 AA; 42876 MW; D031BB48B29F08EF CRC64;

Query Match 36.1%; Score 657; DB 6; Length 378;
Best Local Similarity 38.9%; Pred. No. 4.9e-49;
Matches 143; Conservative 65; Mismatches 122; Indels 38; Gaps 7;

QY 5 QNOSTDYEEENKNGTYDYSOYELICIKEDVEBAKFLPVLITVIVIGLAGNSMVA 64
Db 25 QNOSTDYEEENKNGTYDYSOYELICIKEDVEBAKFLPVLITVIVIGLAGNSMVA 81
QY 65 IYAYKQRTKTDYIINLAVADLLFLTPPMVAVNHGVLGKIMCKITSALYTINFV 124
Db 82 IYAYKQRTKTDYIINLAVADLLFLTPPMVAVNHGVLGKIMCKITSALYTINFV 141
QY 125 SGMQPLACISIDRYAVATKVPDSQSGVKPCNICGVMAAILLSIPOLVYTVND 180
Db 142 SGMQPLACISIDRYAVATKVPDSQSGVKPCNICGVMAAILLSIPOLVYTVND 201
QY 181 NA-----RCIPIPRVYLGTSKALIQMLEICIGFVPEFLMGVCYFITAATLMKMPNIXI 235
Db 202 SSSSQMARCCLIEH---VEAFTTIOAVQVIGFVPEFLMGVCYFITAATLMKMPNIXI 258
QY 236 SRPLKVLITVIVITQLPYINIVKFCRAIDIIYSLTSCNMSKRMIDIAQVETALPH 295
Db 259 NKAIVIAVAVVIVITQLPYINIVKFCRAIDIIYSLTSCNMSKRMIDIAQVETALPH 318
QY 296 SCNPIIYVFMGASFKYVYVMAKKGYSWRQSQVSEFPDSEGPTEPTSTPSI 341
Db 319 SCNPIIYVFMGASFKYVYVMAKKGYSWRQSQVSEFPDSEGPTEPTSTPSI 369
QY 342 TEPTSTPSI 349
Db 370 AETTTTTS 377

RESULT 6
Q8CAG2 PRELIMINARY; PRT; 378 AA.

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AC 08C452; 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Chemokine.
GN CCR7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA The Riken Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL EMBL; AK037965; BAC29909.1; -.
DR MGD; MGI:103011; Ccr7.
DR GO; GO:0016493; P:C-C chemokine receptor activity; IMP.
DR GO; GO:0006935; P:chemotaxis; IMP.
DR GO; GO:0006955; P:immune response; IMP.
DR InterPro; IPR001064; Ccrystalin.
DR InterPro; IPR002076; GPCR_Rhodopsn.
DR Pfam; PFO0001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPEN.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 378 AA; 42855 MW; F02745198B59683 CRC64;

Query Match 35.6%; Score 648; DB 11; Length 378;
Best Local Similarity 38.6%; Pred. No. 3e-48;
Matches 140; Conservative 67; Mismatches 128; Indels 28; Gaps 7

OY 5 QNSTDYIYEEENMGTYDSQYIELICKEDYREFAKYFLFVFLITVYVIGLAGSMVYA 64
DB 25 QDEVLTDDYIGENT--TDVITYLESVCFRKDVRFKAFPLMYSVICFVGLNGVLTLL 81
OY 65 IYAVYKORTKDTVYTLNLAVALDLFLPLFWANAVAHGVAVLQKIMCKTTSALYTLNFV 124
DB 82 TIYIFKRLKMTDITYLNLAVADILFLILPFWASPAKSIIFSVYLCKIISGITYLTSF 141
OY 125 SGWQFLACISIDRYVAVTVPs---QSGVGKPCWIIICFWMAAILLSIPOLVFYTVND 180
DB 142 SGMLLLICSIDRYVAIVQAVSAHHRARVLLISLTSQVGIWMLDLFLSIPELLVGLQK 201
OY 181 NA-----RCIPRPRLVIGTSMAL--IQMLEICGFVYVPLIMVCVFITARTLMMPNI 233
DB 202 NSGEDTLRC---SLVSAQVETALLTITVOAQWQFELVEMLANSCYLLIITRLLQARNF 256
OY 234 KISRPLEKLTIVIVIVITVLPYNIIVKRCRAIDITYSLTSCNNSKMDIAIQVETSIAL 293
DB 257 ERKKAKIVIIAAVVVAVTIFQLPYNQVLAQYVANENITNSCERSKQNLIAVDVTSLS 316
OY 294 FHSLLNPILYVFMGASFKYVYVKKYAKKGSRRQK-----QVVEFPDSDGPIEPFS 346
DB 317 VRCCVVFELVAFGVKFRSDLEKRLKRDIGCLSQERLRHWSSCRHVNASVSMK--AETTT 374
OY 347 TFS 349
DB 375 TFS 377

RESULT 7
ID 086151 PRELIMINARY; PRT; 380 AA.
AC 086151;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

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DE Chemokine receptor 7.
GN CCR7.
CC Sus scrofa (Pig).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RA SEQUENCE FROM N.A.
RA Shinkai H., Muneta Y., Awata T., Uenishi H.;
RT "Molecular cloning and chromosomal assignment of swine chemokine
RL receptor 7 (CCR7).";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Shinkai H., Muneta Y., Awata T., Uenishi H.;
RT "Molecular cloning and mapping of swine chemokine receptor 7 (CCR7).";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB090816; BAC57561.1; -.
DR EMBL; AB090812; BAC57929.1; -.
DR EMBL; AB090810; BAC57929.1; JOINED.
DR EMBL; AB090811; BAC57929.1; JOINED.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPS.
DR PROSITE; PS00225; CRYSTALLIN_BETA_GAMMA; 1.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_F_2; 1.
DR Receiver.
SQ SEQUENCE 380 AA; 42851 MW; 948B2794C6A76AD8 CRC64;
Query March 35.5%; Score 645.5; DB 6; Length 380;
Db Matched Local Similarity 37.3%; Pred. No. 4; 9e-48;
Matches 140; Conservative 73; Mismatches 119; Indels 43; Gaps 9;
QY 1 MALEQNSTDYEEENEMNGTYDYSQYELICIKEDVEPAKVLPLPLTVITVIGLAGNS 60
DB 22 VCLCODEVTDYIGDNT---TVDYTTLVESVCFKXDVTFKAMEFLPVWYSIIICFVGLGNG 78
QY 61 MVAVALVYVYKQKPKEDVTLNLAVADLLLLFTLPFAVNAVHGMVLGKIMCKTSLALYT 120
DB 79 LVMLTYTFEKLKMTDTYTLNLAVADLLPLTLFPWYSAKSWGVGHYCKILFGIYK 138
QY 121 LNFVSGMQLACISIDRYVAVTKVPS---QSGVGEKMWIICFCVMAAILISIPQVLEY 176
DB 139 ISFSGMLLLCLSIDRYVAIVQAVSHRRARLTLSKLSGVCIGIMLAWLSPPELLYS 198
QY 177 TVADNA-----RCIPRPRIYLGISMKL--IQMLEICIGFVPPPLNGVCFFIARTLMK 229
DB 199 GTOKSSSEQALRC-----SLITEHVELLITIQVAMVGFLIPVAWSFCFLVIRILLQ 253
QY 230 MNKIKSRPLKVLTVIVFVLTQLPYNIVKFCRAI-DIYSLITSGMSKEMDIAQVTV 288
DB 254 ARNERKRAIKVIAVAVVFAVAPQLPFGVLAQTVANFNITSGTSCSLKQMLAVCVT 313
QY 289 ESIALFHSCLNPIIIVFMGASFKNYVWKVAKKG-----SV-----RROQSVEEF 334
DB 314 YSLACVACVNPFLYAFYAGVFRSDLFKTLFIDGLCLSOERLRQWSRCRHTRRSSMSAE-- 371
QY 335 PFDESGTEPTSTPS 349
DB 372 -----AETTTTTS 379

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DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DE 01-OCT-2003 (Tremblrel. 25, last annotation update)
DR Chemokine receptor CCR9 (CC chemokine receptor 9A).
GN CCR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99248139; PubMed=10229797;
RA Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
RT "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the
RT receptor for the chemokine TECK."
RN J. Immunol. 162:5671-5675 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Yu C.-R., Peden K.W.C., Farber J.M.;
RT "CCR9A and CCR9B, Two Receptors for the Chemokine CCL25 (TECK/Ckbeta-
RT 15).";
RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132337; CAB43477.1; -.
DR EMBL; AF145439; AAF66699.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR004069; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO1531; CHEMOKINER9.
DR PROSITE; PS00237; GPCR_RHODOPSIN.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 369 AA; 42015 MW; F27CEACFB6844C CRC64;

Query Match 35.3%; Score 643; DB 4; Length 369;
Best Local Similarity 36.4%; Pred. No. 7,9e-48;
Matches 120; Conservative 75; Mismatches 117; Indels 18; Gaps 4;

QY 6 NOSTDYEE-NEMNGTYDSQYELICIKEDYREPAKFLPVFLTVFVIGLAGSMVVA 64
DB 12 NMADVGSSSTSMEDYVNFNFTDFCEKNVRQFASHFLPLVYLTVFVIGLAGSLVIL 71
QY 65 IAYYKQRTKTDVYLINAVADLLFLTPMAVNAVHGVLGKIMKITSALTALFV 124
DB 72 VYVYCTRVKMTDMFLNLAIADLLFLVLPFWAIAADQMKQFTMCKVANSMTKMEY 131
QY 125 SGWQFLACISIDRYVAVTVKPSQSGVGKPCW-----IICFVMAAILLSIPOLVF 175
DB 132 SCVLLMCLISVDRYIAIQ-----AMRAHTKREKLLYSKMCFTIIVLAALCPEILY 186
QY 176 YTVNDN---ARCIPIFRYLGTSKALIQMLEICIGFVFPILMGVCYITRTIMKEN 232
DB 187 SQIKESGIALCTMVPSPDESTKLKSAVLTLLKVLIGFLPFVMAACCTIIIIHTLIQAK 246
QY 233 IKTSRLKVLTVVIVIVITQLPYIVKFCRAIDIIYSLTSCNMSKMDIAIQTESIA 292
DB 247 SSGKALKKTIITVIVFVLSQFPYNCILVQITDAAMTISNCAVSTNIDICQVOTIAT 306
QY 293 LEHSCINPILVFMGASFKNYVMKVAKKYG 322
DB 307 FFHSCINPVLVYFVGERFRDLVKTLKNG 336

RESULT 9
Q8CH33 PRELIMINARY; PRT; 369 AA.
AC Q8CH33;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, last sequence update)

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DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
DE Chemokine receptor CCR9.
GN CCR9.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=LEW; TISSUE=Thymus;
RA Cugini D., Norris M., Remuzzi G.;
RT "Rattus norvegicus chemokine receptor CCR9."
RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458780; AAN76889.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR004069; GPCR_Rhodopsn.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO1531; CHEMOKINER9.
DR PROSITE; PS00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR KX Receptor.
SQ SEQUENCE 369 AA; 41977 MW; 9935561D95FC52C CRC64;

Query Match 35.3%; Score 643; DB 11; Length 369;
Best Local Similarity 36.3%; Pred. No. 7,9e-48;
Matches 119; Conservative 76; Mismatches 111; Indels 22; Gaps 5;

QY 10 DYVYEEENMGTY---DYSQYELICIKEDYREPAKFLPVFLTVFVIGLAGSMVVA 66
DB 16 DYSIDSTASTDDYNNLNFSSF--FCKANNVRQFASHFLPLVYLTVFVIGLAGSLVIL 73
QY 67 AYYKQRTKTDVYLINAVADLLFLTPMAVNAVHGVLGKIMKITSALTALFV 126
DB 74 WYCTRVKMTDMFLNLAIADLLFLVLPFWAIAAQWQFTMCKVANSMTKMEYSC 133
QY 127 WQFLACISIDRYVAVTVKPSQSGVGKPCW-----IICFVMAAILLSIPOLVF 177
DB 134 VLLMCLISVDRYIAIQ-----AKAQWRKRLYSKMCFTIIVLAALCPEILY 188
QY 178 VNND---ARCIPIFRYLGTSKALIQMLEICIGFVFPILMGVCYITRTIMKEN 234
DB 189 ISGSGIALCTMVPSPDESTKLKSAVLTLLKVLIGFLPFVMAACCTIIIIHTLIQAK 248
QY 235 ISRLKVLTVVIVIVITQLPYIVKFCRAIDIIYSLTSCNMSKMDIAIQTESIA 294
DB 249 HKKALKKTIITVIVFVLSQFPYNCILVQAVDAVTMFSNCTISTNIDICQVOTIAT 308
QY 295 HSCINPILVFMGASFKNYVMKVAKKYG 322
DB 309 HSCINPVLVYFVGERFRDLVKTLKNG 336

RESULT 10
Q9R1V0 PRELIMINARY; PRT; 367 AA.
AC Q9R1V0.
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
DE CC chemokine IARC specific receptor.
GN CCR6 OR CCKBR6 OR MCCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RA Tanaka Y.;
 RT "Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor
 for CC Chemokine LARC";
 RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB016031; BAA82443.1; -
 DR MBL; MGI:1333797; Ccr6.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR InterPro; IPR004067; CC_6_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO1529; CHEMOKINER6.
 DR PRINTS; PRO0237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW RECEPTOR.
 SQ SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6D3 CRC64;
 Query Match 33.6%; Score 611; DB 11; Length 367;
 Best Local Similarity 38.2%; Pred. No. 4,8e-45;
 Matches 130; Conservative 60; Mismatches 124; Indels 26; Gaps 8;
 QY 8 STDYEEENKNGYDSQYELI-----CIKEDVREFAKVELFVFLITVFVGLAGNSM 61
 DB 3 STESYFGTDD---YDNTVEYSIPPDHQPCLSEVRNFTKVFIAYSLICVGLGNIM 58
 QY 62 VVAIYAYKKORTKTDVYILNLAVADLLFLTFPMNAV-NAHGVMVGKIMCKITSLYT 120
 DB 59 VVMTFAFKKRSMTDVLNLMAITDILFVTLFPMAVTHATNWSDAICLMKGTVA 118
 QY 121 LNFVSGMFLACISIDRYAVATKVPSSGSGVKPCW---IICFCVMAAILLSIPOLVF- 175
 DB 119 VNENGMMLLACISMDRYAIVQATKSPRVSRRLTHSKVICAVWFSLIISSEPIFN 178
 QY 176 --YVNDARCLPIFPRVLGTS---MALLQMEICIGFVFPFLINGVCYFTARTLMK 229
 DB 179 KKEYQDQDVC--EPRRYSVSEPTWELGLGEFFGFTPLFVFCYCLFIKLVQ 235
 QY 230 MPNIKSRPLKLVIVFIVTQLPYNIYKFCRAIDIIYLSITSCMSKMDIAIOVTE 289
 DB 236 AONSGRHAIRVAVAVLFLACQIPHNMLLVLRVN-TGVNARSCTEKLAVATRVAAE 294
 QY 290 SIALFHSCLNPLIYFNGASFKNYMKAKKYGSRORQ 329
 DB 295 VLAFLHSLNPLVLAFLIQKFRNYFMKIMKDVCMCRKXK 334
 RESULT 11
 ID 042444 PRELIMINARY; PRT; 368 AA.
 AC 042444;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Chemokine receptor
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OC NCBI_TaxID=8022;
 RX MEDLINE=98260342; Pubmed=10331499;
 RA Daniels G.D., Zou J., Charlemagne J., Partula S., Cunningham C.,
 RA Secombes C.J.;
 RT "Cloning of two chemokine receptor homologs (CXC-R4 and CC-R7) in
 RT rainbow trout Oncorhynchus mykiss.";
 RL J. Leukoc. Biol. 65:684-690 (1999).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AJ003159; CA05917.1; -
 DR GO; GO:0016021; C:receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO0237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 SQ SEQUENCE 368 AA; 41523 MW; 328E2D4C47B821A CRC64;
 Query Match 32.2%; Score 586.5; DB 13; Length 368;
 Best Local Similarity 37.3%; Pred. No. 6,5e-43;
 Matches 120; Conservative 58; Mismatches 125; Indels 19; Gaps 4;
 QY 22 YVYSQY-----ELICKEDVREFAKVELFVFLITVFVGLAGNSVVAIYAYK 70
 DB 17 YDYSSEFPPTGDEDVDNPMCKSAVRARFGQYEBPLWYSVILGLGNLVVMIYHFR 76
 QY 71 KQ-RTKTDVYIILNLAVADLLFLTFPMNAVNAHGMVVGKIMCKITSLYTLNFPVSGNQF 129
 DB 77 QRLKMTMDIYLLNLAVADLFLGLTFLWAVEANQMSFGLGCKVTSAFYKINFFSSMLL 136
 QY 130 LACISIDRYAVATKVPSSGSGVKP---CWIIICFCVMAAILLSIPOLVFYVND---NA 182
 DB 137 LTCISDRIYVIVQTTVAQNSKQRLSCSKFVCACVILLAVLALPEFMFANVXELDQF 196
 QY 183 RCIPFPRVLGTSKMALIQMLEICIGFVFPFLINGVCYFTARTLMKPNIKSRPLKVL 242
 DB 197 YCTMYTWSNQNRRTKIVIVGLQICMGFCPLVWVFCAGIIRTLKRSFQKHALLVVI 256
 QY 243 LVVIVFIVTQLPYNIYKFCRAIDIIYLSITSCMSKMDIAIOVTEIALFHSCLNPL 302
 DB 257 LVVAVVAVLSQLPYNSVVMETQANSTQTDCAAKRNVSVQLKSLIYTHACLNPL 316
 QY 303 YVFMGASFKNYMKAKKYGSM 324
 DB 317 YVFGVRFRRDILKLRITHCM 338
 RESULT 12
 ID 08HZ87 PRELIMINARY; PRT; 374 AA.
 AC 08HZ87;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE CC chemokine receptor 6.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OC NCBI_TaxID=9544;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Choi Y.K., Fallert B.A., Murphey-Corb M.A., Reinhart T.A.;
 RT "Simian Immunodeficiency Virus Dramatically Alters Expression of
 RT Homeostatic Chemokines and Dendritic Cell Markers During Infection In
 RT Vivo";
 RL Blood 0:0-0(2002)
 DR EMBL; AF508730; AAN47098.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR004067; CC_6_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO1529; CHEMOKINER6.
 DR PRINTS; PRO0237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW RECEPTOR.
 SQ SEQUENCE 374 AA; 42649 MW; A64A515BAC9E928 CRC64;


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Db      12 DGHVEGDWLFNNSDSSQ-----ENKRFLEKREVFLEPCVYLVVFGLGSLVLI 64
QY      66 YAYVKORRTDQVYLLNLAVADLLFLPFMAVANAHVAGVIGKINCKITSALYTLNFS 125
Db      65 YIFVYKRTLDVFLNLPLADLVFVCTLPFMAVAGTEVVEFGVTCRTLRGMTNNFV 124
QY      126 GMOFLACISIRYAV--TKVPSQSGVGRPCW--IIFPCVMAAILLSIFQVLFYVND 180
Db      125 SMLTLCTIVRFVIVVQATGAFNRQAKWK--IMGVQICLLIIVVSLVSLPQIIYGHVQD 183
QY      181 NARCIPIPRRYLGTSMKALLIQMLEICIGFVVPFLIMGVCFYITARTLMKPNIKISRLPK 240
Db      184 IDKI---QYHSEISITMVLVIQWTLGFFLPFLMLICYSGLIKTLLHARNPQKHSLK 240
QY      241 VLLTVYVFIYVQLPYNTVVKFCRAIDIIYSLITSGNSKRDIAIQVTESTALFHSCLNP 300
Db      241 IIFLVVAVFLLQTFPFLNLAFLMIQSTSWERYTITS-----FKYALVTEALAYFRACINP 294
QY      301 ILVYFMGASFKNYVMKAKRYG-----SMRRQSQVEEPFDESGPTEPTSTPSI 350
Db      295 VLYAVFGKFRKNVWKMKDKIGCLSHGVSSQWKSSBDSK--TCSASHNVEITSMFOL 351

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RESULT 15

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Q9BDS6 PRELIMINARY; PRT; 343 AA.
ID Q9BDS6
AC Q9BDS6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 24, Last annotation update)
DE Orphan seven transmembrane receptor STRL33.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBT_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2134756; PubMed=1124524;
RA Wade-Evans A.M., Russell J., Jenkins A., Javan C.;
RT "Cloning and sequencing of cynomolgus macaque ccr3, gp15, and strl33:
RT potential coreceptors for HIV type 1, HIV type 2, and STV."
RU AIDS Res Hum Retroviruses 17:371-375(2001).
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF291671; AAK25742.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007166; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 343 AA; 39472 MW; 0961328F948E7784 CRC64;

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Query Match 31.1%; Score 566; DB 6; Length 343;
 Best Local Similarity 33.1%; Pred. No. 3.7e-41;
 Matches 118; Conservative 73; Mismatches 133; Indels 32; Gaps 8;

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QY      10 DYVYEENMNGTYDYSQYELICIKEDVREFAKVFLEPVFLTVFVIGLAGNSMVAATYAY 69
Db      5 DHYEDDGLNSPNDSSQEE---HQDFLQFRKVFPCMYLVVFVCGLVGNSLVVLSIFY 60
QY      70 KKQRTKTVYILNLAVADLLFLPFMAVANAHVAGVIGKIMCKITSALYTLNFSGMQF 129
Db      61 HRLQSLTVFLVNLPLADLVFVCTLPFWTYAGIHFWIGQVWCKTLGVTYINFTSMLI 120
QY      130 LACISIDRYVAVTKVPS--QSGVGKPCW--IIFPCVMAAILLSIPQVLFYV--NDNAR 183

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Db      121 LNCITVDRIIVVYKATKANKQAKMTNGKVCILIMVISLVSIPQIIYGVNVLDKLI 180
QY      184 CIPFPRYIGTSMKALLIQMLEICIGFVVPFLIMGVCFYITARTLMKPNIKISRLKYL 243
Db      181 C-----GYHDEISITVVLATQWTLGFFLPFLAMICYGVIIKTLLHAGGFQGRRLKII 235
QY      244 TVYIVFIVYVQLPYNTVVKFCRAIDIIYSLITSGNSKRDIAIQVTESTALFHSCLNP 303
Db      236 LVNAVFLQLQTFPFLNLAFLMIQSTSWERYTITSFHYT-----IIVTEALAYFRACINP 289
QY      304 VFMGASFKNYVMKAKRYG-----SMRRQSQVEEPFDESGPTEPTSTPSI 350
Db      290 AFVSLKFRKNFWKLVKDIGCLPYLGVSQWKSSBDSK--TFSASHNVEATSMFOL 343

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Search completed: April 13, 2004, 13:16:21
 Job time : 47 secs